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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ubiquitous nuclear receptor - used to develop prods. for use in diagnostic, drug design and therapeutic applications.
                                                      Adn12168
Abm82160
Abm82160
Abb18851
Abb54183
Abb57053
Abb57053
Abb05731
Abb05731
Abb05735
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Ady51560 1
Abr83627
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             AAW25034
AAR96215
ADK85628
ABR82544
ABR82544
ABR82544
ADN12168
ABW8216
ABW8210
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AAR33744
ABP60037
ADYS1560
ABR83627
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Liao S, Song C;
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Aar97982 F
Aar98140 N
Abg31015 F
Adj14182 F
Adp05729 F
Adq48625 V
              Compugen Ltd
                                 - protein search, using frame plus n2p model
     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compug
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                2443163 segs, 439378781 residues
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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geneseqp2001s:*
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                                                                                                                                                                             GInGinLeuvalAlaAlaGlnLeuGlnCysAsnLysArgSerPheSerAspGlnProLys
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Matches:
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Best Local Similarity:
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DB:
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identify steroid hormone agonists and antagonists.
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87. .154
/note= "DNA binding
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                                                                                   Steroid hormone receptor; NERI
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N-PSDB; AAQ63134.
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Binding-site
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Pred. No.:
                                                                                                             Homo sapiens
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Steroid receptor NER (AAR97982) is a novel member of the nuclear receptor family. Its amino acid sequence was deduced from a gene (AAT18996) isolated from a human osteosarcoma SAOS-2/B10 cell library. A COS stable expression system allows prodn. of recombinant NER. NER is useful for identifying cpds. which act e.g. as potentiators of NGF, muscarinic agonists or dopamine D1 antagonists. TOFA (5-tetradecyloxy)-2-furan carboxylic acid) was found to activate NER and to be a potent potentiator
                                                                                                                                                                                              AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATC
                                                                                                                                                                                                                                                                                                           GlnGlySerSerSerSerAlaSerGlyProGlyAlaSerProGlyGlySerGluAlaGly
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5; Page 54-57; 72pp; English.
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                                                                                                                                           TICITGAG-GACTICACCTACAGCAAGACGACTICCACCGIGCAGGCCTGCAGGTGGAG
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                                        GTGCCTGGTTTCCTGCAGCTGGGCCGGGAGGACCAGATCGCCCTCCTGAAGGCATCCACT
                                                                                                                                                                                                                                                                                                                                                                     NGF potentiator; muscarinic agonist;
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87. .154
/note= "putative double zinc finger structure"
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(MEDI-) MEDICAL COLLEGE PENNSYLVANIA.
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N-PSDB; AAT18996.
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360

288 420 308 480 328 348 599 368 408

300 268

188

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LX receptor beta; LXRB; targeting construct; transgenic animal; diabetes; impaired glucose tolerance; reduced blood insulin level; hypoactivity;
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SerGlnGlySerGlyGluGlyGluGlyValGlnLeuThrAlaAlaGlnGluLeuMetlle
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                                                                   CAGCAGTTGGTGGCGGCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAA
                                                                                                                                                            GTCACGCCCTGGCCCCTGGCCGCAGACCCCCAGTCCCCGAGATGCCCGCCAGCAACGCTTT
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31-JUL-2001; 2001US-0309404P.
10-DEC-2001; 2001US-00013823.
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ABG310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel human steroid hormone receptor (AAR98140), designated NER, is useful as a potentiator of ligands for other receptors, partic. G-protein coupled receptors. It was identified as the product of a DNA clone (AAT30031) isolated from an osteosarcoma SAOS-2/B10 library. Recombinant NER can be obtd. using a COS expression system. Cpds. that activate the NER receptor, such as TOFA (5-(tetradecyloxy)-2-furan carboxylic acid), potentiate the effects of nerve growth factor and may be useful in treatment of Alzheimer disease. They may also potentiate the effects of muscarinic agonists in the treatment of ocular hypertension, or dopamine bliopamine D1 antagonists in the treatment of psychoses and movement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATC 180
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                                                                                                                                                                                                                                                                                                G-protein coupled receptor; nerve growth factor; Alzheimer disease; ocular hypertension; schizophrenia; distonia; tardive dyskinesia; Gilles de la Tourette syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oid hormone receptor NER activators - for potentiating modulator of G-protein coupled receptor.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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           IleLysArgProGlnAspGlnLeuArg
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1231.00
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99.60$
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                                                                                                    protein;
                                                                                                                                                                                                                                                                              potentiator;
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                                                                                                                                                                                                                                 NER receptor potentiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI ) MERCK & CO INC. (MEDI-) MEDICAL COLLEGE
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N-PSDB; AAT30031.
                                                                                                                                                                                       (first
                                                                                                 AAR98140 standard;
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                                                                                                                                                                                                                                                                                receptor;
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           409
                                                                                                                                              AAR98140;
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GAGTACGCCCTGCTCATCGCCATCAACATCTT
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                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                             MILLER A.
MOORE J T.
MOORE L.
WILLIAMS S P.
                                                                                                                                                                                                                                                                                                                                                       BLEDSOE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-224393/21.
                                                                                                                                                                                                                                LXR beta; receptor.
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                    369
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                                                                                                                       RESULT
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                                                                                  The invention describes a new targeting construct (I) comprising a first polynucleotide sequence homologous to a LX receptor beta (LXRB) gene, a second polynuclectide sequence homologous to the LXRB gene and a selectable marker. (I) is useful for producing transgenic animals, preferably mice having a disruption in the LXRB gene, that may be used as models for disease, e.g. diabetes. The transgenic animals methods are useful in identifying agents that modulate LXRB function used for disquosing, treating or ameliorating conditions associated with LXRB function, e.g. impaired glucose tolerance, reduced blood insulin levels, hypoactivity or lethargy. This is the amino acid sequence of the human LX receptor beta (LXRB), an RXR (retinoid X receptor) interacting protein
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                 New targeting construct useful for producing transgenic animals with a disruption in the LX receptor beta (LXRB) gene that may be used in treating or ameliorating conditions associated with LXRB function, e.g. diabetes or hypoactivity.
                                                                                                                                                                                                                                                                                                                                                                       AGCCAGGGCTCCGGGGGAAGGCCAGGGTGTCCAGCTAACAGGGGCTCAAGAACTAATGATC
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                   Example 1; Fig 3A; 62pp; English.
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99.60%
WPI; 2002-590736/63
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crystalline form useful for designing modulator that modulates activity of nuclear receptor polypeptide, comprising substantially pure liver X receptor ligand binding domain polypeptide, ligand, and/or coactivator polypeptide.
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                                                                                                                                                                                                         Claim 44; SEQ ID NO 4; 198pp; English.
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121 AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATC
bone; joint; breast; immune system; metabolic;
                                                                            12-NOV-2003; 2003WO-US036229
                                                                                            14-NOV-2002; 2002US-0426305P
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 pancreas; bone; joint; br
nutritive disease; human.
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                                                                                                              (NURA-) NURA INC.
                                                                                                                                                                N-PSDB; ADP05730
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                                                                                                                               Gaitanaris GA,
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                          Homo sapiens.
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                                           GlnGlySerSerSerSerAlaSerGlyProGlyAlaSerProGlyGlySerGluAlaGly
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This invention relates to a novel method of determining whether a patient has an increased risk for developing a disease or disorder which comprises determining the presence of a mutation or polymorphism in the patient. See the patient or measuring the patient or in a cell of the patient. The invention may colypeptide in the patient or in a cell of the patient. The invention may be useful for the development of compounds with an antibacterial, antithyroid, cardiovascular-Gen, cytostatic, dermatological, eatingmanisoraters-Gen, gastrointestinal-Gen, gynaecological, hepatotrophic, insorders-Gen, gastrointestinal-Gen, gynaecological, hepatotrophic, immunosuppressive, muscular-Gen, nephrotrophic, osteopathic or virucide activity. The method is useful for determining whether a patient has an increased risk for developing a disease or disorder. The nucleic acid cencoding a nuclear receptor polypeptide, an expression vector comprising the nuclear acid operably linked to a promoter, or a compound that the muclear acid operably linked to a promoter, or a compound that condulates the biological activity of a nuclear receptor polypeptide, is useful for treating or preventing a disease or disorder of the adrenal gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular, cy vary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid, uterus, pancreas, bone and joints, breast, or immune system, or metabolic or nutritive disease or disorder. The present sequence is that of a nuclear receptor protein which may be used in the method of the
                                                                                                                                                                                                                                                                                   Determining an increased risk for e.g. colon, brain or breast disease or disorder, by detecting a mutation or polymorphism in the nuclear receptor gene, or measuring expression or biological activity level of the nuclear
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Zeng H;
3A, Bergmann JE, Gracerov A, Hohmann J, Mcilwain KL, Pavlova MN, Vassilatis D,
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                                    screening assay.
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SerGlnGlySerGlyGluGlyGluGlyValGlnLeuThrAlaAlaGlnGluLeuMetIle
             TTCATCAACCCCATCTTCGAGTTCTCGCGGGCCATGCGGGGGCTGGGCCTTGAACGCT
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                                         GICACGCCCTGGCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCGCCAGCAACGCTTT
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The invention relates to a crystal comprising at least 150 amino acid residues of the liver X receptor beta (LKRbeta) ligand binding domain. The ligand binding domain preferably comprises amino acid residues Ser242. Phe268, Phe214, Thr272, Leu274, Ala275, Ser278, Ile309, Met312, Leu313, Glu315, Thr316, Arg319, Ile327, Phe329, Leu330, Tyr335, Phe340, Leu449, Leu453, Trp457, according to the co-ordinate tables or homologue of the molecule or molecular complex, where the homologue has a root mean square deviation form the backbone atoms of the amino acids of not more square deviation form the backbone atoms of the amino acids of not more of the amino acid 220-461 of the 461 LKRbeta protein. The crystal is useful in X-ray crystallography, and for drug screening assays. This sequence corresponds to the full length human LXRbeta protein.
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at least 150 amino acid residues useful in X-ray crystallography,
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                                                                                    Claim 31; SEQ ID NO 1; 378pp; English
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ew crystal comprising igand-binding domain,
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GInGInLeuvalAlaAlaGInLeuGInCysAsnLysArgSerPheSerAspGInProLys
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AAGATTCGGAAACAGCAGCAGCAGCAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG
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                                           388
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                                                              PhelleAsnProllePheGluPheSerArgAlaMetArgArgLeuGlyLeuAspAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening lipid metabolism or insulin resistance improvement drug contacting test substance with cell capable of controlling ABCA1 expression, analyzing change in liver X receptor dependent transcriptional activity.
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Matches:
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                                                                                                                                                                                                                                        Human LXR protein - SEQ ID 12.
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N-PSDB; AEB94509.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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PhelleAsnProllePheGluPheSerArgAlaMetArgArgLeuGlyLeuAspAspAla 368
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Therefore screening for ECDN and ECDNsm protein binding mols., using recombinant ECDN and ECDNsm proteins will be useful in the identification of candidate anticancer drugs. Gene expression of ECDN and ECDNsm proteins in normal and cancerous tissues can be studied using primers and probes derived from ECDN and ECDNsm protein cDNA. Antibodies which
                                                                                                                                                                                                                                                                                                                                                                                                                           289 ValProGlyPheLeuGlnLeuGlyArgGluAspGlnIleAlaLeuLeuLysAlaSerThr 308
                                             ATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
                                                                         TTCTTGAG-GACTTCACCTACAGGAGGACGACTTCCACCGTGCAGGCCTGCAGGTGGAG
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                                                                                                                                                                                                                                                                                                               GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; foetal lung; steroid hormone; receptor; analogue protein;
ECDN protein; carceris screening; binding molecule; recombinant;
identification; anticancer drug; cancerous tissue; primer; probe;
antibody; immunohistochemical assay.
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N-PSDB; AAT27616.
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                                                                                                                                                                                                                                                                                                                    The invention relates to a combination comprising CDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a CDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a CDNA. The sample is from a subject with the wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow the combination with molecules or compounds under conditions to allow compensions. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepstitis. The present sequence represents a human protein which is differentially expressed in steroid-induced C3A liver cells. Note: The sequence data for this patent did not form part of the printed control of the printed sequence in the printed sequence has a second of the printed sequence has a second of the printed sequence data for this patent did not form part of the printed sequence has a second of the printed sequence has a second of the printed sequence data for this patent did not form part of the printed sequence has a second of the printed sequence ha
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                                                                                                                                                                    Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises CDNAs that are differentially expressed in response to steroid
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12-OCT-2000; 2000US-0240409P
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1227.00
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                                                                                    Buchbinder JL;
                                           (INCY-) INCYTE CORP
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                                                                                      Furness LM,
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Pred. No.:
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 recognise ECDN and ECDNsm Inmunohistochemical assays
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                                                                                                                                                                                                                                                                                                                                                                           AAW25034 shows the amino acid sequence of a human ubiquitous nuclear receptor polypeptide (UR). The UR is useful in assays designed to select substances which interact with the UR which may potentially be of use therapeutically. UR is also used in diagnosis and drug design. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGGCCG
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                          therapy;
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                          domain;
                       receptor polypeptide; DNA binding
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Human ubiquitous nuclear receptor polypeptide
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   ECDNsm protein cDNA. Antibodies which recognise ECDNsm proteins used in ECDNsm protein immunohistochemical assays
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Matches:
Conservative:
Mismatches:
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1221.00
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Best Local Similarity:
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GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG
                                                                                                                                                                                                            CCGGGCCGCGTGGAGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGTCCTACACGCGC
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                                                                            TTCTTGAG-GACTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCCTGCAGGTGGAG
                                                                                                                      Human; foetal lung; steroid hormone; receptor; analogue protein; ECDN protein; cancer; screening; binding molecule; recombinant; identification; anticancer drug; cancerous tissue; primer; probe; antibody; immunohistochemical assay; variant; small molecule; ECDNsm.
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Pyridone, antilipemic; antidiabetic; antiarteriosclerotic; litholytic; hepatotropic; antisebortheic; dermacological; antiparkinsonian; cardiant; nootropic; neuroprotective; antilnflammatory; cytostatic; anorectic; cardicovascular; nephrotropic; antithyroid; ophthalmological; hypotensive; cerebroprotective; immunosuppressive; nuclear receptor; liver X receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGGCCGCGTGCAGGCGTTGCAGCAGCCCTACGTGCAGGCGCTGCTGTCCTACACGCGC 719
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hypercholesterolemia, hyperlipoproteinemia, hyperglycemia, diabetes
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                                                   inflammatory bowel disease; LXRbeta; nuclear hormone receptor; metabolism; cholesterol; pharmaceutical; Crohns disease; ulcerative colitis; colitis; ischemia; gastrointestinal-gen.; antiinflammatory; antiulcer; receptor.
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                           Human LXRbeta protein.
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N-PSDB; ADX85627.
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mellitus, dyslipidemia or atherosclerosis,

invention relates to N-substituted pyridone compounds of Disclosure; Page 517-519; 544pp; English. $\mathbb{E} \times \mathbb{E} \times$

The invention Frances to Arsubstituted Compounds to a pretitured formula. The compounds act as modulators of nuclear receptor, orphan nuclear receptors and liver X receptor (LXRalpha or LXRbeta). They are useful for the treatment, prevention or ameliotration of symptoms of conclear receptor mediated diseases or disorders which are modulated or affected by nuclear receptor activity or in which nuclear receptor activity is implicated e.g. hypercholesterolemia, hyperlipoproteinemia, hypertriglyceridemia, lipodystrophy, hyperglycemia, disbetes mallitus, dyslipidemia, atherosclerosis, gallstone disease, acne vulgaris, conditions with conditions, diabetes, parkinson's disease, acneer, inflammation, immunological disorders, lipid disorders, obesity, conditions characterized by a perturbed epidermal barrier contitions characterized by a perturbed epidermal barrier contitions characterized by cholesterol, triglyceride or bile of a disease or disorder affected by cholesterol, triglyceride or bile contitions of hyspocholesterolemia and in vitro method for altering nuclear receptor activity. The compounds are also used to reduce cholesterol levels, modulates cholesterol metabolism, increase concentrate (ABC1) in the cells. The compounds are also useful for the treatment of macrovascular disease, connary contexpendised. Hypothyroidism, renal failure. The present sequence represents con human LXR beta polypeptide

can bumman LXR beta polypeptide

Sequence 460 AA

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.39e-91 1215.50 99.20% 99.20% 88.46% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-10-712-629B-2 (1-746) x ABR82544 (1-460)

187 120 207 180 SerGlnGlySerGlyGluGlyGluGlyValGlnLeuThrAlaAlaGlnGluLeuMetIle 227 240 247 300 267 GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA 360 287 480 121 AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGGCTCAAGAACTAATGATC CAGCAGTTGGTGGCGCCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAA GTCACGCCCTGGCCCCTGGGCGCAGACCCCCAGTCCCCGAGATGCCCCGCCAGCAACGCTTT 1 AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG 241 301 61 208 181 228 요 a 8 ద 셤 ò 셤 ò ò 원 ò ò ઠે

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Search completed: November 25, 2005, 22:22:56 Job time : 172 secs

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Cyaccession: JC4014
R;Shinar, D.M.; Endo, N.; Rutledge, S.J.; Vogel, R.; Rodan, G.A.; Schmidt, A.
Gene 147, 273-276, 1994
A;Title: NRR, a new member of the gene family encoding the human steroid hormone nuclea
A;Reference number: JC4014; MUID:95011628; PMID:7926814
A;Accession: JC4014

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C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Oct-2004
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A,Cross-references: GDB:389570; OMIM:600380
A,Map position: 19q13.3-19q13.3
C;Keywords: steroid hormone receptor
F;85-381/Domain: erbA transforming protein homology *
F;87-154/Domain: DNA binding #status predicted *BIN>
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-Q=/cgn2_1/USPTO spool p/USIO112629/runat_25112005_143037_11006/app_query.fasta_1.903
-Q=/cgn2_1/USPTO spool p/USIO112629/runat_25112005_143037_11006/app_query.fasta_1.903
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-ODCALLGN=200 -THR SCORE=pc- THR MAX=100 -TRANS=human40.cdi -LIST=45
-OOTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=USI0712629 @CGN 1 1 63 @runat_25112005 143037_11006 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGS_SCORES=0 -MAXLT -DSPBLACK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TNESUME -NGS_CORES=1 -XGAPEXT=0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Database

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C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C; Accession: 149021
E; Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol, 9, 72-85, 1995
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
R;Teboul. M; Emmark, E; ii, Q; Wikstrom, A.C.; Pelto-Huikko, M.; Gustafsson, J.A.
R;Title: OR-1, a member of the nuclear receptor superfamily that interacts with the 9-ci
A;Recession: 159354
A;Recession: 159354
A;Recession: 159354
A;Recession: 1-446 <RES
A;Cross-references: UNIFROT:G62755; UNIPARC:UPI000013050B; EMBL:U20389; NID:g665941; PIC
A;Reperimental source: Sprague-Dawley, Hepatic
R;Song, C.; Kochtis, J.M.; Hilpakka, R.A.; Liao, S
Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994
A;Title: Ubiquitous receptor: a receptor that modulates gene activation by retinoic acid
A;Reference number: 159264; MUID:95062154; PMID:7971966
A;Recession: 159264
A;Returns translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPARC:UPI0000145BB3; EMBL:U14533; NID:g565661; PIDN:AAA52361.1;
A;Experimental source: vagina
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A;Molecule type: mRNA
A;Residues: 1-32,'V',34-51,55-218,'V'.2
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Secies: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 0.10ec-1995 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004
C;Accession: A56043
R;Apfel, R.; Benbrook, D.; Lernhardt, B.; Ortiz, M.A.; Salbert, G.; Pfahl, M.
A;Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive el
A;Reference number: A56043; MUID:95021230; PMID:7935418
A;Accession: A56043
A;Accession: A56043
A;Residues: 1-445 <APF
A;Molecule type: mRNA
A;Residues: 1-445 <APF
A;Accessiones: UNIPROT:062685; UNIPARC:UPI000013050D; GB:U11685; NID:9555751; PIDN
A;Residues: authors translated the codon GAG for residue 73 as Ser
C;Keywords: steroid hormone receptor; zinc finger
C;Keywords: steroid hormone receptor; zinc finger
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718.50
75.40%
60.89%
52.29%
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Best Local Similarity:
Query Match:
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                                                                           NID:9691713;
A; Title: Isolation of proteins that interact specifically with the retinoid X ;
A; Reference number: A57664; MUD: 95280959; PMID: 7760852
A; Accession: 14908:
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-446 < RES>
A; Cross-references: UNIPROT: Q60644; UNIPARC: UP100000281D3; EMBL: U09419; NID: g6; Genetics:
C; Genetics: RIPIS
C; Keywords: zinc finger
F; 76-366/Domain: erbA transforming protein homology < RRBA>
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Length:
Matches:
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Mismatches:
Indels:

Gaps:

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360 272 420 480

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A;Cross-references: UNIPROT:P49882; UNIPARC:UP1000050DEA; GB:S60739; NID:g385893; PIDN A;Note: sequence extracted from NCBI backbone (NCBIN:132124, NCBIP:132127) C;Keywords: DNA binding; steroid hormone receptor; zinc finger F;113-432/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                   Cyspecies: Chironomus tentans
Cybecies: Chironomus tentans
Cybecies: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 31-Dec-2004
Cybecession: A56590
Insect Biochem. Mol. Biol. 23, 115-124, 1993
AyTitle: Cloning of a Chironomus tentans CDNA encoding a protein (cEcRH) homologous 1A; Reference number: A56590; MuID:93250857; PMID:8485513
A; Accession: A56590
A; Accession: A56590
A; Molecule type: mRNA
A; Residues: 1-536 < IMH>A; Residues: 1-536 < IMH
A; Residues:
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                                                                                                    TTCATCAACCCCATCTTCGAGTTCTCGCGGCCATGCGGCGGCTGGGCCTGGACGACGCT
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 16-Peb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Oct-2004
C; Accession: 138975
R; Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
Genes Dev. 9, 1033-1045, 1995
A; Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
A; Reference number: 138975; MUID: 95262897; PMID: 7744246
A; Retaus: preliminary
A; Rotatus: preliminary
A; Molecule type: mRNA
A; Residues: 1-447 <RES>
A; Cross-references: UNIPROT: Q13133; UNIPARC: UP100000529F2; EMBL: U22662; NID: 9726512; E; 96-367/Domain: erbA transforming protein homology <RENA>
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                                              373 GlnLeuGlnValGluArgLeuGlnHisThrTyrValGluAlaLeuHisAlaTyrValSer 392
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11	630 TICTCGGCCGACCGACGTGCAGGAGCCGGGCGGCGTGGAGGCGTTGCAGCAGCCC 68		
299 LyePyContileschaptorintriedidityIntr	430 PheserAspargProGlyLeuGluLysAlaGluMetValAspIleIleGlnSerTyr 44	495	
0	690 TACGTGGAGGCGCTGCTGCTAC		
December	449 TyrThrGluThrLeuLysValTyr	555	
0.5-0ct-2004 0.5 0	RESULT 7 JC7230	314	
December	vitamin D receptor subtype b - Paralichthys olivaceus C:Species: Paralichthys olivaceus	615	
The composition of the composi	ø	334	
December of Flower December December December of Municipal ManyFiledinicHHisHisPicoly 373	Risuzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T. Riocham Biochus Das Ormana 270 40-48 2000	675	
Decrease and bone formatic Aviose Passage Passag	min D receptor in	354	
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costasis and bone formatic RESULT 8 RESULT 8 RESULT 8 RESULT 8 Recipent - fruit fly (Drosophila melanogaster) Copate: 30-70m-1992 facquence_revision 30-70m-1992 facet. Change 31-Dec-2004 Copate: 30-70m-1992 facquence_revision 40-70m-1992 factor 40-70m-1992 fact	A;Residues: 1-425 <suz> A;Cross-references: UNIPROT:Q91B74; UNIPARC:UP100000FCBB4; DDBJ;AB037674</suz>	374 GlyArgleu	
cidyanome receptor - fruit [14] (Inceaphila melanogaster) Cidhes: 3-Uur.1992 sequence_revision 30-Jun-1992 flext_change 31-Dec-2004 Airtic = Inceaphila ER gane encodes an ecideone receptor, a new member of the Airtic = Inceaphila	eostasis and bone formati		
Content of Content o		Godysone receptor - fruit fly (Drosophila melanogaster)	
Rikecle, W. R.; Talbot, W. S.; Segraves, W. A.; Bender, M. T.; Cherbas, P.; Hogness, D. A; Higher Trainbot, M. S.; Segraves, W. A.; Bender, M. T.; Cherbas, P.; Hogness, D. A; Higher Trainbot	itamin	Jun-1992 #text_change	4
1.56=-14 Langth: 425 Arceleation Alloss Arc		A.; Bender, M.T.; Cherbas,	ogness, D.S.
Conservative 4	1.96e-14 Length: 287.00 Matches:	n ecdysone receptor,	of
10	45.63% Conservative: 28.90% Mismatches:	A. Accession: A41055 A; Molecule type: mRNA	
10	20.89% Indels: 2 Gaps:	C:UPI00001246E6; GB:M74078;	9157317; PIDN
12 GAGGGGGCGCAGGCGAAGGCGAAGGCGTCCAGGAA 171	(1-746) x JC7230	exon boundaries ly expressed at the end of the	hird larval i
11	112 GAGGCAGGCAGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAA	C.Genetica: A,Gene: FlyBase:EcR	
172 CTAATGATCCAGCGACTGCAACTGCAGTGCAACTGCACTCTCCAGC 21			
134 Glnvailiehlametieuvalduuliahishispischtryzaspaspeiryzseitäp 139 Glnvailiehlametieuvalduuliahishispischtryzaspaspeiryzseitäp 139 Glnvailiehlametieuvalduuliahishispischtryzaspaspeiryzseitäp 139 Glnvailiehlametieuvalduuliahishispischtryzaspaspeiryzseitäp 139 Glnvailiehlametieuvalduuliahispischtryzaspaspeiryaspei	172 CTAATGATCAGCAGTTGGTGGCGGCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGAC	hormone receptor; n homology <erba></erba>	regulation; z
232	134 GlnVallleAlaMetLeuValGluAlaHisHisLysThrTyrAspAspSerTyrSerAsp	2 525-14 Tonoth.	
154 PheCyakagheArgProProValArgGluGlyProValThrArgSerAlaSerNagSerAlaSerNagSerAlaSerNagSerAlaSerNagSerAlaSerNagSerAlaSerNagSerAlaSerNagNala 173 Best Local Similarity: 31.724 Mismatches: 87 Mismatches: 52 Gaps: 9 Gaps:	232CAGCCCAAAGTCACGCCCTGGCCCCTG	285.50 Matches: 48.51% Conservative:	
13 AlaSerLeuNisSerSerAspSerPheSerHisSerProGluSer 193 08-10-712-629B-2 (1-746) x A41055 (1-878) 08-10-712-629B-2 (1-746) x A41055 (1-878) 08-10-712-629B-2 (1-746) x A41055 (1-878) 09-10-712-629B-2 (1-746) x A41055 (1-878) 10-712-629B-2 (1-746) x A41055 (1-878) 11-878 11-878	154 PheCysArgPheArgProProValArgGluGlyProValThrArgSerAlaSerArgAla	31.72% Mismatches: 20.78% Indels:	
259	174 AlaSerLeuHisSerLeuSerAspAlaSerSerAspSerPheSerHisSerProGluSer	(1-746) x A41055 (1-878)	
	259GGCGCAGAC		69
268 CCCCAGTCCCGAGATGCCTTGCCCACTTCACGGAGCTG 318 214 ProAspSerSerFaluGluGluGlySerSerPheSerMetLeuProHisLeuAlaAspLeu 233 315 GCCATCAGTCCGAGATGCCTGGTGGATCTGAGGAGCTGGGCAGGAGCCTGGTGGATCTGAGGAGCAGGAGGCAGCAGGAGGCTTCCTGAGGAGCTTCCTGAGGAGGCTTCGAGGAGGCTTCGAGGAGGCTCAA	: : : 194 ValAspThrLysValAsnPheAsnAsnLeuLeuMetMetTyrGlnGluGlnGlySerSer	e.	366
319 GCCATCAGTCCAGGAGATCGTGCAAGTGCTGGTTTCCTGCAG 378 319 GCCATCAGTCCAGGAGGTTCCAGGAAGGCTTCCTGCAG 378 319 GCCATCAGTCCAGGAGGTTCCAGGAAGGCTTCCTGCAG 378 310 GCCATCAGTCCAGGAGGTTCCAGGTAACTGCTGGTTTCCTGCAG 378 311 GCCATCAGTCCAGGAGGAGGTTCCAGGTTAAACTGCTCAGGTAAACTGCTAGGTTAAAAAAAA	268 CCCCAGTCCCGAGATGCCCGCCAGCAACGCTTTGCCCACTTCACGGAGCTG 318	70 AGCAGCTCAGCCTCTGGGCCTGGGGCTTCCCCTGGTGGATCTGAGG	
127 GGCTCCGGGGAAGGCTGCGTTCCAGGGAAGGCTGCGGGTTCCAGGTTCCAGGGTTCCAGGGTTCCAGGTTCCAGGGGTTCCAGGGGGCCCAACTGCAGGTTCCAGGGGCCCAACTGCAGGTCCAACGGTTCCTTCC	114 FLOASDOCTSCLOLUGIUGIUGIUGIUGIUGIUGIUGIUGUFUURULUGURIGUGUALAABDUGU 233	36/ AsnGıySerLewAlaSerGıy	
379 CTGGGCCGGGACGACCACATCGCCTCCTGAAGGCATCCACTATCGAGATCATGCTGCTA 438 Qy 169GAACTAATGATCCAGCAGTGGAGGCCCAACTGCAGTGCAACAAACGCTCCTTC 22	319 GCCATCATCTTCAGGAGATCGTGGACTTGGCTAAGTAGTGGCTGGTTTCTTGCAGGAGATCTTGCTGCAGATGCTAAGTAAG	377	168 396
	379 CTGGGCGGGAGACCAGATGCCCTCCTGAAGGCATCCACTATCGAGATCATGCTGCTA 43	169	22

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A;Accession: A31761
A;Accession: A31761
A;Accession: A31761
A;Accession: A31761
A;Residues: 1-423 <BRNA
A;Residues: 1-423 <BRNA
A;Cross-references: UNIPROT: P13053; UNIPARC: UP100001382C3; GB:J04147; GB:J03630; NID:g2
R;Burmester, J.K.; Maeda, N.; Debuca, H.F.
Broc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988
A;Title: Isolation and expression of rat 1,25-dihydroxyvitamin D-3 receptor cDNA.
A;Reference number: A31367; MUD:88124963; PMID:2829212
A;Accession: A31367.
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C;Species: Rattus norvegicus (Norway rat)
C;Dacession: A31761, A31367
R;Burmester, J.K.; Wiese, R.J.; Maeda, N.; DeLuca, H.F.
Proc. Natl. Acad. Sci. US.A. 85, 9499-9502, 1988
A;Tille: Structure and regulation of the rat 1,25-dihydroxyvitamin D-3 receptor A;Reference number: A31761, MUID:89071726; PMID:2849110
                      :::||| ||| :::
123 ArgLeuAsnGluGluGlnAlaArgMetIleSerSerLeuValGluAlaHisHisHysThr
                                                                                                                                                          :::|||
162 ValThrArgSerAlaSerArgAlaAlaSerLeuHi8SerLeuSerAspAlaSerSerAsp
                                                                                                                                                                                                                                                                                                                                                  222 LeuproHisLeuAlaAspLeuValSerTyrSerIleGlnLysVallleGlyPheAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                 242 MetileProGlyPheArgAspLeuThrAlaGluAspGln1leAlaLeuLeuLy8SerSer
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                                                                 AACAAACGCTCCTTCTCCGACCAGCCCAAAGTCACGCCCTGGCCCCTGGGCGCAGACCCC
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362 IleArgileAsnHisProGlyGlyArgLeu 371
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A;Residues: 'R',58-423 <BU2>
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C;Species: Paralichthys olivaceus
C;Species: Paralichthys olivaceus
C;Species: Op-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 05-Oct-2004
C;Accession: JC7229
R;Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Blophys. Res. Commun. 270, 40-45, 2000
A;Title: Identification of CDNAs encoding two subtypes of vitamin D receptor in flounder
A;Reference number: JC7229
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------ProSerLeuThrTyrAsnGlnLeuAlaValIleTyrLysLeuIleTrpTyr
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      ---LysCysGlnAlaArgAsnIle
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A;Experimental source: intestine
C;Comment: This receptor is an important factor in calcium homeostasis a
                                                                                                       ----GACCCCAGTCCCGAGATGCCCGCCAG----
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        397 IleProLeuLeuProAspGluIleLeuAla---
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transport;
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C; Keywords: bone; calcium
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A; Residues: 1-420 <SUZ>
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Best Local Similarity:
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ProGlyValGlnAspAlaLysLeuValGluAlaIleGlnAspArgLeuSerAsnThrLeu 359
       C;Superfamily: Vitamin D3 receptor (VDR); exbA transforming protein homology C;Keywords: DNA binding; transcription regulation; zinc finger F;24-137/Domain: extbA transforming protein homology <ERBA> F;24-44/Region: zinc finger F;60-84/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitamin D receptor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Oct-2004
C;Accession: PC4019
E;Kamei, Y.; Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, E. Gene 152, 281-282, 1995
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Matches:
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Best Local Similarity:
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'Vitamin D receptor isoform A - Japanese quail

Cybaceies: Coturnix coturnix japonica (Japanese quail)

Cybaceies: I3-Sep-1996 #sequence_revision I3-Sep-1996 #text_change 05-Oct-2004

Rystlatous: Isofasti M.A.; Prahl, J.M.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994

Ayritle: The avian vitemin D receptors; primary structures and their origins.

Ayreference number: I50451; MUID:95062315; PMID:7972109

Ayreference number: I50451; MUID:95062315; PMID:7972109

Ayreference number: I50451

Ayreferences: MNA

Ayreferences: UNIPROT:P49701; UNIPARC:UPIO0001382C2; EMBL:U12641; NID:9595500; PI
A,Title: Cloning and sequencing of the gene encoding the mouse vitamin D receptor.

A,Reference number: PC4019, MUID:95137405, PMID:7835717

A,Accession: PC4019

A,Molecule type: mRNA

A,Residues: 1-422 «KMN»

A,Cross-references: UNIPROT:P48281, UNIPARC:UP100000272E6; DDBJ:D31969; NID:g699618; IC,Superfamily: Vitamin D3 receptor (VDR)

C,Reywords: DNA binding; zinc finger
F;22-336/Domain: erbA transforming protein homology «ERBA»
F;24-89/Domain: DAA binding #status predicted «BIN»
F;191-422/Region: vitamin D binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 GACTICGCTAAGCAAGIGCCTGGTTICCTGCAGCTGGGCCGGGAGGACCAGATCGCCCTC 405
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LeuLysSerSerAlaIleGluValIleMetLeuArgSerAsnGlnSerPheThrMetAsp 277
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| AspMet9erTrpAspCysGlySerGlnAspTyrLysTyrAspIleThrAspValSerArg 297
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ArgProGlyValGlnAspAlaLysLeuValGluAlaIleGlnAspArgLeuSerAsnThr 357
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LeuGlnThrTyrIleArgCysArgHisPro 367
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CiSpecies: Homo sapiens (man)
CiDate: 19-May-1999 #sequence_revision 19-May-1989 #text_change 05-Oct-2004
CiAccession: A28200; 155353
Ribaker, A.R.; McDonnell, D.P.; Hughes, M.; Crisp, T.M.; Mangelsdorf, D.J.; Haussler, M.
Froc. Natl. Acad. Sci. U.S.A. 85, 3294-3298, 1988
A;Title: Cloning and expression of full-length cDNA encoding human vitamin D receptor.
A;Reference number: A28200
A;Accession: A28200
A;Accessi
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218 Thr------BeuGluLeuSerGlnLeuSerMetLeuPro
                                                             184 CAGTIGGIGGCGCCCAACIGCAGIGCAACAAACGCICCTICTCCGACCAGCCCAAAGIC
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A;Molecule type: mRNA
A;Residues: 24-90 <RES>
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C; Species: Rattus norvegicus (Norway rat)
C; Accession: S24174
C; Accession: S24174
R; Goto, H.; Chen, K.; Prahl, J.M.; Deluca, H.F.
Biochim. Biophys. Acta 1132, 103-108, 1992
A; Title: A single receptor identical with that from intestine/T47D cells mediates the A; Reference number: S24174; MUID:92379083; PMID:1324736
A; Resident type: mRNA
A; Residents: L427 < GOTS-A; Residents: R54174; MUID:92379083; PMID:1324736
A; Residents: L427 < GOTS-A; R64017-A; R640
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|HisLeuAlaAspLeuValSerTyrSerIleGlnLysValIleGlyPheAlaLysMetIle
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C;Superfamily: Vitamin D3 receptor (VDR)
C;Keywords: DNA binding; transcription regulation; zinc finger
F;22-341/Domain: erbA transforming protein homology <ERBA>
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C;Superfamily: Vitamin D3 receptor (VDR)
C;Keywords: zinc finger
F;42-362/Domain: erbA transforming protein homology <ERBA>
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390 CysArgHisPro 393
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C;Species: Kenopus laevis (African clawed frog)
C;Date: 04-Mar.1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: A41977
                                                                                                                                                                                                                       SerSerSerSerCysSerAspHisCys---IleThrSerSerAsp-----MetMetAsp
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A Cross-references: GDB:120487; OMIM:601769; OMIM:277440
A;Map position: 12412-12414
C;Superfamily: Vitamin D3 receptor (VDR); erbA transforming protein C;Keywords: DNA binding; transcription regulation; zinc finger F;22-341/Comain: erbA transforming protein homology <ERBA>
F;24-44/Region: zinc finger
F;60-84/Region: zinc finger
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Matches:
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R;Blumberg, B.; Mangelsdorf, D.J.; Dyck, J.A.; Bittner, D.A.; Evans, R.M.; De Robertis, Proc. Natl. Acad. Sci. U.S.A. 89, 2321-2325, 1992
A;Title: Multiple retinoid-responsive receptors in a single cell: families of retinoid A;Reference number: A41977; MUID:92196110; PMID:1312717
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284 MetThrPheSerAspGlyLeuThrLeuAsnArgThrGlnMetHisAsnAlaGlyPheGly 303
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|AspalaGluThrGlyLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeu 342
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| GlnGluThrPheProAlaLeuCysGlnLeuGlyLysTyrThrThrSerPheSerSerGlu
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Kiauaner R.D., Colling F.S., Wagner L.H., Schenen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heidh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Oxysterols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (Nuclear receptor NER).
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044337_9ACAR
044337_9ACAR
046297_GECLA
076246_UCAPU
04W6D0_LEPDE
097095_LOCMI
0671184_CARMA
002035_TENNO
002035_TENNO
04TU03_PIG
NR1H3_RAT
051035_RAT
051035_RAT
051036_RAT
051031_RAT
051031_RAT
051031_RAT
051031_RAT
061013_RAT
061011_CHICK
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O77240 CHOFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=NR1H2; Synonyms=LXRB, NER, UNR;
   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
 NCBI_TaxID=9606;
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TO NR1H2 HUMAN
719.5
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 Command line parameters:
-MODEL=frame+ 1.099 (JUSIO712629/runat_25112005_143036_10996/app_query.fasta_1.903
-MODEL=frame+ 1.0p.model_-DF/USIO712629/runat_25112005_143036_10996/app_query.fasta_1.903
-DB=Uniprot -QFWT=fastan_-SUPFIX=n2p.rup -MINMATCH=0.1 -LÖOPCL=0 -LÖOPEXT=0
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -ALIGN=15 -MODE=LOCAL
-OCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pco -NORM=ext -HEAFSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USRE=USIO712629 @CGN 1 1 466 @runat_25112005 143036_10996 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSP // THREOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPUEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                        - protein search, using frame_plus_n2p model
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0618BU6 HUMAN

068CY8 HUMAN

058D83_BOVIN

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081BP65_MOUSE
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1: uniprot_sprot:*
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Maximum DB seq length: 2000000000
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1374
1 aagattcqqaaacac
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Xgapop 10.0 , Xç
Ygapop 10.0 , Yç
Fgapop 6.0 , Fç
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C. -I FUNCTION: Orphan receptor. Binds preferentially to double-stranded of oligonucleotide direct repeats having the consensus half-site of sequence 5.-AGGTGA.3 and 4-nt spacing (DR-4).

C. -SUBUNIT: Forms a heterodimer with RXR.

C. -SUBCELIGLAR LOCATION: Unclear (Potential).

C. -TISSUE SPECIFICITY: Ubiquitous.

C. -SIMILARITY: Belongs to the nuclear hormone receptor family. NRI

C. -SIMILARITY: Contains 1 nuclear receptor DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R GO; GO:0005634; C:nucleus; TAS.

R GO; GO:0003677; F:DNA binding; TAS.

R GO; GO:0004879; F:Idpand-dependent nuclear receptor activity; TAS.

R InterPro; IPR001628; Hrmn.rcpt_lig_bd.

R InterPro; IPR001023; Stdhrmn.receptor.

R InterPro; IPR001034; VitD_receptor.

R InterPro; IPR001034; VitD_receptor.

R Pfam; PF00104; Hormone recept.

R Pfam; PF00105; Zf-C4; I.

R PRINTS; PR00138; STROIDFINNER.

R PRINTS; PR00138; STROIDFINNER.

R PRINTS; PR00139; Zi C4steroid; 1.

R PROSTITE; PS00011; NUCLEAR_REC_DBD_1; 1.

R PROSTITE; PS1030; NUCLEAR_REC_DBD_1; 1.
                                                                                                   human
                                                                                                                                                                         NUCLECTIDE SEQUENCE OF 7-461.
Song C., Konkontis J.M., Hijpakka R.A., Liao S.;
Widquitous receptor: a novel receptor that modulates gene activation by retinoic acid and thyroid hormone receptors.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 209-461 IN COMPLEX WITH
                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U07132; AAA61783.1; -; mRNA.
EMBL; BC007790; AAH07790.1; -; mRNA.
EMBL; BC047760; AAH07790.1; -; mRNA.
EMBL; BC04750; AAH47500.1; -; mRNA.
EMBL; U14534; AAA58594.1; -; mRNA.
PIR; JC4044; JC4014.
PDB; 1P8D; X-ray; AB=214-461.
PDB; 1PQC; X-ray; AB=214-461.
PDB; 1PQC; X-ray; AB/C/D=213-461.
PDB; 1PQC; X-ray; AB/C/D=213-461.
PDB; 1PQC; X-ray; AB/C/D=213-461.
PDB; 1UPV; X-ray; AB/C/D=213-461.
PDB; 1UPV; X-ray; AB/C/D=213-461.
PDB; 1UPW; X-ray; AB/C/D=213-461.
PDB; UPW; X-ray; AB/C/D=213-461.
PDB; UPW; X-ray; AB/C/D=213-461.
PDB; UPW; X-ray; AB/C/D=213-461.
PDB; UPW; X-ray; AB/C/D=213-461.
                                                                                                                       mouse cDNA sequences."
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GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCGGGAGATCGTGGACTTCGCTAAGCAA 360
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Transcription regulation, Zinc, Zinc-finger.
161 Nuclear receptor.
107 NR C4-type.
                 NR C4-type.
NR C4-type.
Ligand-binding (Potential).
Poly-Gen.
                                                                      68CE3D9F9BC5C0BE CRC64;
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Matches:
Conservative:
Mismatches:
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480

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289 ValProGlyPheLeuGlnLeuGlyArgGluAapGlnIleAlaLeuLeuLyBAlaSerThr 308
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                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                         CAGCAGTTGGTGGCGGCCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAA
                                                                                                                                                                                 GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA
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GO:0005634; Cinucleus; IEA.
GO:0046872; F:metal ion binding; IEA.
GO:0003707; F:steroid hormone receptor activity; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO:0006350; P:transcription; IEA.
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-!- SUBCELLUIAR LOCATION.
-!- SUBCELLUIAR LOCATION: Wuclear (By similarity).
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
EMBL, CR456706; CAG32987.1; -; mRNA.
HSSP: P20393; 1A6X.
SMR; Q61BU6; 220-460.
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Last sequence update)
Last annotation update)
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InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR000324; VitD_receptor.
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
NRIHZ protein.
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QEIBUG;
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wangner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Rab Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M.J., Ubdin T.B., Toshiyuki S., Carminci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gaibbs R.A.,

RA Holards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muxy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratesley R.W., Touchman M., Maran M.A.;

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A. C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A. Schein J.B., Jones S.J.M., Marra M.A.;

Rad mouse cDNA sequences.",

Rad mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
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                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JULY 2002) to the EMBL/GenBank/DDBJ databases.

1. SUBCELLULAR LOCATION: Nuclear (By similarity).

1. SINGELLULAR LOCATION: Nuclear (By similarity).

2. SINGLARITY: Belongs to the muclear hormone receptor family.

EMBL, BC033500; AAH33500.1, -, mRNA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:eraroid hormone receptor activity; IEA.

GO; GO:0003700; F:ranscription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DNA-hinding; Metal-Dinding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc.; Zinc.-finger.

SEQUENCE 461 AA; 51102 MW; 68CE3D9F9BCSCOBE CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Nuclear receptor subfamily 1, group H, member 2.
Name=NR1H2;
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Matches:
Conservative:
Mismatches:
Indels:
  461 AA
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QSIOY1 HUMAN PRELIMINARY;
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TISSUE=Brain;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity:
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RUCLEOTIDE SEQUENCE.
TISSUE=Endometrium carcinoma cell line;
THOGENTIDE SEQUENCE.
THE German CDNA Consortium;
The German consortium;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686D1580.
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98.41%
86.54%
                                                                            QEBCYB HUMAN PRELIMINARY;
Q68CY8;
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                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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Best Local Similarity:
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InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; Hormone_recep; 1.
Pfam; PF00105; zf-c4; 1.
PRINTS; PR00398; ZTRDHORMONE.
PRINTS; PR00350; ZTRDHORMONE.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00047; STROIDFINGER.
PROMITS; SM00430; VITAMINDR.
SMART; SM00430; Znf_C4steroid; 1.
SMART; SM00399; Znf_C4; 1.
SMART; SM00399; Znf_C4; 1.
SMART; SM0039; Znf_C4; 1.
SMART; SM0031; WUCLEAR REC_DBD_1; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 461 AA; 51087 WW; 697E3D9F9BC5COBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGlnGlySerGlyGluGlyGluGlyValGlnLeuThrAlaAlaGlnGluLeuMetIle
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Matches:
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1231.00
99.60%
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Best Local Similarity:
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-1-SIMILARITY: Belongs to the nuclear hormone receptor family.
-1-SIMILARITY: Belongs to the nuclear hormone receptor family.
-1-SIMILARITY: Belongs to the nuclear hormone receptor family.
-1-SIMILARITY: Belongs to the nuclear hormone receptor factor.
-1-SIMILARITY: Belongs to the nuclear hormone receptor factor.
-1-SIMILARITY: Belongs to the nuclear hormone receptor activity; IEA.
-1-SIMILARITY: F: metal ion binding; IEA.
-1-SIMILARITY: F: metal ion factor activity; IEA.
-1-SIMILARITY: F: metal ion factor in factor activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;

Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,

Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.

Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,

Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,

Keele J.W.;
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Q58D83.
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Nuclear receptor subfamily 1, group H, member 2.
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MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Nuclear receptor subfamily 1, group H, member 2.
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QSBINI 10-MAY-2005 (TYEMBLEE). 30, C:
10-MAY-2005 (TYEMBLEE). 30, L:
10-MAY-2005 (TYEMBLEE). 30, L:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RMR; OSBIS6; 214-454.

RILLEPPO; IPRO01228; Hrmm_rcpt_DNA_bd.

InterPro; IPRO01228; Hrmm_rcpt_DNA_bd.

InterPro; IPRO01228; Hrmm_rcpt_Dad.

RILLEPPO; IPRO01224; VitD_receptor.

RILLEPPO; IPRO01324; VitD_receptor.

RRINTS; PRO0139; ZIPC-C4; I.

RRINTS; PRO0139; ZIPC C4; I.

RRINTS; PRO0130; NUCLEAR REC_DBD_1; I.

RRINTS; PRO0130; NUCLEAR REC_DBD_2; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.,
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                            Oxysterols receptor LXR-beta.

Name-NR1H2;

Name Box faurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lauraslatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 nuclear receptor DNA-binding domain.
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Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                        13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                           455 AA
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Matches:
  CGCATCAAGAGCCGCAGGACCAGCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BT021148; AAX31330.1; -; mRNA.
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Query Match:
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TTTGCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG 357
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ThrPheLeuLysAspPheThrTyrSerLysAspAspPheH18ArgAlaGlyLeuGlnVal 341
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              IleGlnGlnLeuValAlaAlaGlnLeuGlnCyaAsnLysArgSerPheSerAspGlnPro 241
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Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101; Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T., Casas B., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L. Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J., Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Lauraaiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle.";
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databages.
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Nuclear receptor subfamily 1, group H, member 2.
Name=NR1H2;
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Q58CP4;
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PRINTS; PR00398; STREDHORMONER.
PRINTS; PR003950; VITAMINDR.
SWART; SW00430; DOLL; 1.
SWART; SW00399; ZnF C4; 1.
SWART; SS0031; NUCLEAR REC DBD 1; 1.
PROSITE; PS51030; NUCLEAR REC DBD 2; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
SRQUENCE 455 AA; 49986 MW; 38C9FAC055BCA146 CRC64;
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                                                                                                                                                                                                  T.P.L.;
Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G. Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G., Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J., Keele J.W.;
                                                                     "Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle."; Genome Res. 11:626-630(2001).
                                                                                                                                                                                                                                              Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SINILARITY: Belongs to the nuclear hormone receptor family.
EMBL; BT021193; AAX31375.1; -; mRNA.
                                                                                                                                                                            Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L., Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T. "Sequencing and analysis of Bos taurus full-length insert cDNA
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Matches:
Conservative:
Mismatches:
Indels:
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11144.50
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                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                            GlyValSerSerSerSerProAlaSerGlyProGlyAlaSerProGlyGlySerAspGly
                                                                                                                                                                                                                                                     GGCAGCCAGGGCTCCGGGGAAGGCGAGGTGTCCAGCTAACAGCGGCTCAAGAACTAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BT021903; AXX46750.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00046872; F:netal ion binding; IEA.
GO; GO:0003700; F:steroid hormone receptor activity; IEA.
GO; GO:0003700; F:remerription factor activity; IEA.
GO; GO:0005350; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:rranscription; IEA.
Transcription regulation; IEA.
Transcription regulation; Sinclear protein, Receptor; Transcription; SEQUENCE 498 AA; 54139 MW; 29CED3E4E6F44156 CRC64;
                                                                                                                                                                                   AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG
                                                                                                                                                                                                                                                                                                                     AAAGTCACGCCCTGGCCCCTGGGCCCCAGACCCCCGAGATGCCCGCCAGCAACGC
                                                                                                           Length:
Matches:
Conservative:
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Indels:
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1144.50
94.80%
94.00%
83.30%
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PROSITE; PS51030; NUCLEAR_REC_DBD_2, 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                             062755; 062694;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2000 (Rel. 48, Last sequence update)
Oxysterols receptor LixP-beta (Liver X receptor beta) (Nuclear orphan receptor LixP-beta) (Ubiquitously-expressed nuclear receptor) (UR)
Name=Nrlh2; Synonyms=Lxxb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITINE 55062154; PubMed=1971966; Song C., Kokontis J.M., Hitpakka R.A., Liao S.; Song C., Kokontis J.M., Hitpakka R.A., Liao S.; Fubiquitous receptor: a receptor that modulates gene activation by retinoic acid and thyroid hormone receptors."; Proc. Natl. Acad. Sci. U.S.A. 91:10809-10813(1994).
-!- FUNCTION: Orphan receptor. Binds preferentially to double-strand oligonucleotide direct repeats having the consensus half-site sequence 5'-AGGTCA-3' and 4-nt spacing (DR-4).
-!- SUBUNIT: Forms a heterodimer with RXR.
-!- SUBUNIT: Belongs to the nuclear hormone receptor family. NRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Spraque-Dawley, TISSUE-Liver;
MEDLINE=95199298; PubMed=7892230;
Teboul M., Enmark E., Li Q., Wikstrom A.C., Pelto-Huikko M.,
Gustafsson J.-A.;
Gustafsson J.-A.;
with the 9-cis-retinoic acid receptor.";
Proc. Natl. Acad. Sci. U.S.A. 92:2096-2100(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 nuclear receptor DNA-binding domain.
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EMBL; U1453; AAA52361.1; -; mRNA.
PIR; 15934; 159354.
HSSP; P55055; 1P8D.
SMR; O62755; 205-445.
TRANSFAC; T04451; -.
Ensembl; ENSRNOG000019812; Rattus norvegicus.
RGD; 61906; Nr1h2.
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InterPro; IPR000536; Hrmn rcpt lig_bd.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR00324; VitD_receptor.
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PRINTS; PR0047; STROIDFINGER.
PRINTS; PR00350; VITAMINDR.
ProDom; PD000035; Znf C4steroid; 1.
SMART; SM00430; HOLI; 1.
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Pfam; PF00105; zf-C4; 1.
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EMBL; U09419; AAC52164.1; -; mRNA.
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Nuclear receptor.

NR C4-type.

NR C4-type.

Ligand-binding (Potential).
Poly-Gln.

Poly-Pro.
G -> V (in Ref. 2).

Missing (in Ref. 2).
A -> V (in Ref. 2).
A -> V (in Ref. 2).
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Matches:
Conservative:
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92.77%
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80.13%
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Best Local Similarity:
 75
116
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162
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133
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                                                                Alignment Scores:
 DNA_BIND
ZN_FING
ZN_FING
ZN_FING
COMPBIAS
COMPBIAS
COMPBIAS
CONFLICT
CONFLICT
SEQUENCE
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STRAINS-C57BJ/6; TISSUE-Brain;

RAD NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

REDLINE-2538255; FubMed=12477932; DOI=10.1073/pnas.242603899;

RAD Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopking R.F., Jordan H., Moore T., Max J.L., Wang J., Haidh F.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunacatne P.H.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci B., Nullahy S.W.,

Richards S., Worley K.C., Hale S., Garcinces S., Sanchez A.,

Raber J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Raber J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Radriguez A., Sohein J.E., Jones S.J.M., Marra M.A.;

Generation and initial analysis of more than 15,000 full-length human
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                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
0xysterols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan receptor LXR-beta) (Ubiquitoualy-expressed nuclear receptor) (Retinoid X receptor interacting protein No.15).
Name=Nrlh2; Synonyms=Lxrb, Ripls, Unr, Unr2;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontcolires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/SvJ; TISSUB=Liver;
MEDLINE=20156373; PubMed=10675677; DOI=10.1016/S0378-1119(99)00555-7;
Alberti S., Steffensen K.R., Gustafsson J.-A.;
"Structural characterisation of the mouse nuclear oxysterol receptor genes LXRalpha and LXRbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95280959; PubMed=7760852; DOI=10.1210/me.9.1.72;
Seol W., Choi H.S., Moore D.D.;
"Isolation of proteins that interact specifically with the retinoid
receptor: two novel orphan receptors.";
Mol. Endocrinol. 9:72-85(1995).
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-!-FUNCTION: Orphan receptor. Binds preferentially to double-stran oligonucleotide direct repeats having the consensus half-site sequence 5'-AGGTCA-3' and 4-nt spacing (DR-4).
-!-SUBGNIT: Forms a heterodimer with RXR.
-!-SUBCELIDIAR LOCATION: Nuclear (Potential).
-!-TISSUS SPECIFICITY: Ubiquitous.
-!-SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
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STANDARD;
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MOUSE
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274 ValProGlyPheLeuGlnLeuGlyArgGluAspGlnIleAlaLeuLeuLysAlaSerThr 293
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RAMAIN-CSTBL/6J; TISSUE=Whole body;

RAMAIN-CSTBL/6J; TISSUE BODY;

RAMAIN-CSTBL/6J; TISSUE BODY;

RAMAIN-CRAMAIN, Naibhi K., Kiyosawa H., Kondo S., Yamanaka I., Radoca K., Matsuda H.A., Aabhurner M., Batalov S., Casavant T., Radoca K., Matsuda H.A., Aabhurner M., Batalov S., Consavant T., Radoca K., Matsuda H.A., Rabhurner M., Batalov S., Consavant T., Rachim I.M., Staubli F., Suzuki R., Tomica M., Wagner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., Kamiya M., Lee N.H., Ramiya M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Sabaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Schochback C., Saya T., Shibata Y., Schochback Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hayashizaki Y.;

R. Punctional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 8 days embryo whole body CDNA, RIKEN full-length enriched
library, clone:5730478C17 product:nuclear receptor subfamily 1, group
H, member 2, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 PhelleAsnProllePheGluPheSerArgAlaMetArgArgLeuGlyLeuAspAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/61; TISSUE=whole body;
MEDINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                              294 IleGluIleMetLeuLeuGluThrAlaArgArgTyrAsnHisGluThrGluCysIleThr
                                                                                                                                                                                                                                                                                                               TTCATCAACCCCATCTTCGAGTTCTCGCGGCCATGCGGCGGCTGGGCCTGGACGACGCT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentía, Sciurognathi,
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Q8BP65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCCTGGTTTCCTGCAGCTGGGCCGGGACCAGATCGCCCTCCTGAAGGCATCCACT 420
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| PRINTS; PR00399; STRDIDFINGER.
| PRINTS; PR00399; VITAMINDR.
| PRODOM; PD000035; ZIL C4steroid; 1.
| RAMART; SM00430; HOLI; 1.
| RMART; SM00399; ZNF C4; 1.
| RMART; SM00399; ZNF C4; 1.
| RMART; SM00399; ZNF C4; 1.
| RMART; PS00031; NUCLEAR REC DBD 1; 1.
| R PROSITE; PS01031; NUCLEAR REC DBD 2; 1.
| M Transcription regulation; Zinc; Zinc-finger.
| Transcription regulation; Zinc; Zinc-finger.
| TANSTRIC TR 98 NR C4-type.
| TRING 116 140 NR C4-type.
| TRING 116 140 NR C4-type.
| TRING 116 446 Ligand-binding (Potential).
| TRING 116 140 Ligand-binding (Potential).
| TRING 116 POLY-Pro.
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GluProAlaAlaSerSerSerGlyArgProAlaAlaSerProGlyThrSerGluAlaSer 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG
                                                                                                                                                         R TRANSPAC; T04467.

R TRANSPAC; T04467.

R Ensembl; ENSMUSG0000060601; Mus musculus.

R MG1:1352463; Nr1h2.

R GO; GO:0005634; C:nucleus; IDA.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0004879; F:ligand-dependent nuclear receptor activity; IDA.

R GO; GO:00044255; P:regularion factor activity; IDA.

R GO; GO:0004425; P:regularion of transcription, DNA-dependent; IDA.

R InterPro; IPR001528; Hrmn_rcpt_lig_bd.

R InterPro; IPR001528; Hrmn_rcpt_lig_bd.

R InterPro; IPR001328; Yulp_receptor.

R InterPro; IPR001328; Vilp_receptor.

R Pfam; PF00104; Hormone receptor.

R Pfam; PF00105; zf-C4; I
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- I- SUBCELLULAR LOCATION: Nuclear (By similarity).

- I- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/63; TISSUB=Whole body; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Shibata K., Itoh M., Wormalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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PEAM; PF00104; Hormone recep; 1.
PEAM; PF00105; zf-C4; 1.
PRINTS; PR00399; STROIDFINGER.
PRINTS; PR0039; VITAMINDR.
PRINTS; PR0039; VITAMINDR.
PROSTITS; SM00430; VITAMINDR.
SWART; SM00430; LAF C4; 1.
PROSTITE; PS00031; NUCLEAR REC DBD 1; 1.
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SRR, QBRS65; 202-442.

MGI; MGI:11352463; Nr1h2.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0003700; F:transcription factor activity; IDA.

GO; GO:0044255; P:transcription factor activity; IDA.

GO; GO:0044255; P:regulation of transcription, DNA-dependent; IDA.
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InterPro; IPR001723; Schlarm.receptor.
InterPro; IPR00134; VitD_receptor.
InterPro; IPR001628; Znf_C4steroid.
[3]
NUCLECTIDE SEQUENCE.
STRAIN-CS7BL/6J; TISSUE-Whole body;
THE FANTOM CONSOTTIUM,
the RIKEN GENOME Exploration Researd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGGCCGCGTGGAGGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGTCCTACACGCGC 719
                                                                                                                                                                                                                                                                                  SerGlnGlySerGlyGluGlyGluGly1leGlnLeuThrAlaAlaGlnGluLeuMetIle
                                                                                                                                                                                                                                                                                                                                            GINGINLeuValAlaAlaGInLeuGInCygAsnLygArgSerPheSerAggGInProLyg
                                                                                                                                               1 AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG
                                                                                                                                                                                                      AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATC
                                                                                                                                                                                                                                                                                                                           CAGCAGTIGGTGGCGCCCCAACTGCAGTGCAACAACGCTCCTTCTCCGACCAGCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                      GTCACGCCCTGGCCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCGCCAGCAACGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                       TTCTTGAG-GACTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCCTGCAGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATCAACCCCATCTTCGAGTTCTCGCGGGCCATGCGGCGGCGGCTGGGCCTGGACGACGCT
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             222
222
243
243
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                                        Conservative:
Mismatches:
Indels:
             Length:
Matches:
                                                                                                                  US-10-712-629B-2 (1-746) x Q8BP65_MOUSE (1-443)
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                        1095.50
93.57#
89.96#
79.73#
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                                    Percent Similarity:
Best Local Similarity:
Alignment Scores:
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DT HYPOL
GN HYPOL
OS PONGO
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SOW CONTRACTOR OF STANDARD OF

298

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MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.D., Collins F.S., Wagner L.H., Derge J.G.,
A Laschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A prometein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakeeley R.W., Touchman J.W., Garen E.D., Dickson M.C.,
A Blakeeley R.W., Touchman J.W., Garen E.D., Dickson M.C.,
A Rubiting M., Krzywinski M.I., Skalska U., Smailus D.E.,
A schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
A Constrain and initial analysis of more than 15,000 full-length human
----GluileValAspPheAlaLysGln 178
                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                          TICITIGAG-GACTICACCTACAGCAAGGACGACTICCACCGTGCAGGCCTGCAGGTGGAG
                                                                                                                                                                                                                                                                                    TTCATCAACCCCATCTTCGAGTTCTCGCGGCCATGCGGCGGCTGGGCCTGGACGACGCT
                                      GTGCCTGGTTTCCTGCAGCTGGGCCGGAAGGACCAGATCGCCCTCCTGAAGGCATCCACT
                                                                                                                    ATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22341132, PubMed-12454917, DOI-10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGMA2_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.
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A wews H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
A wews H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
- i- SIBCELLULAR LOCATION: Nuclear (By similarity).
- i- SIMILARITY: Belongs to the nuclear hormone receptor family.

EMBL; CRRESTS10; CAHH9793.1; -; mRNA.

EMBL; GREEL4; 140-350.

GO: 00003634; C:nucleus; IEA.

GO: 00003708; F:retinoic acid receptor activity; IEA.

GO: 00003708; F:retinoic acid receptor activity; IEA.

GO: 00003709; F:steroid hormone receptor activity; IEA.

GO: 00003709; F:regulation of transcription, DNA-dependent; IEA.

GO: 00003709; F:ranscription; IEA.

GO: 0000350; P:ranscription; IEA.

InterPro; IPR000536; Hrmon receptor.

InterPro; IPR000324; Vitb receptor.

InterPro; IPR001628; Zif G4steroid.

INTERPRO; IPR001628; Zif G4steroid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCACGCCCTGGCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCGCCAGCAACGCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA 360
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      Chordata, Craniata, Vertebrata, Euteleostomi;
Euarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCAGTTGGTGGCGGCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031; NÜCLEAR_REC_DBD_1, 1.
DNA-binding; Hypothetical protein;
Receptor; Transcription; Transcription requlation; Zinc; Zinc-finger.
SEQUENCE 351 AA; 39475 WW; 175C907978A0247C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351
214
1
1
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31
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO1292; RETNOICACIDR.
PRINTS, PRO0398; STRDHORMONER.
PRINTS; PRO047; STROIDFINGER.
PRINTS; PRO0350; VITAMINDR.
PROMMERT; SMO430; LAIC (48teroid; 1.08mART; SMO430; HOLI: 1.08mART; SMO0399; ZRF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.68e-65
1028.00
86.35%
85.94%
74.82%
                                                                                                                                                  The German cDNA Consortium;
        Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                               NCBI_TaxID=9600;
                                                                                                                               TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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DB:
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TRAIN=Singapore local strain; TISSUE=Embryo;

NEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

B Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

B Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

B Hopkins R.S., Loquellano M.F., Farmer A.A., Rubin G.M., Hong L.,

B Brownstein M.J., Usddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullah S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Hatefield Y.S.N., Krzywinski M.I., Salaka U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG 659
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the nuclear hormone receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein zgc:113339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAAGAGGCCGCAGGACCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                          A Klein S., Gerhard D.S.;

A Klein S., Gerhard D.S.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

L. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

C. -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

B KRID (SCHILD) AAH74169.1; -; mRNA.

R GO; GGO1004684; F:ecdysteroid hormone receptor activity; IEA.

R GO; GGO1004684; F:ecdysteroid hormone receptor activity; IEA.

R GO; GGO1004684; F:ecdysteroid hormone receptor activity; IEA.

R GO; GGO10068496; F:steroid binding; IEA.

R GO; GGO1006350; F:transcription factor activity; IEA.

R GO; GGO1006350; F:transcription factor activity; IEA.

R GO; GGO1006350; F:transcription; IEA.

R InterPro; IPR001324; VitD receptor.

DR InterPro; IPR001324; VitD receptor.

DR Ffam; PF00104; Hormone recep; 1.

DR PRINTS; PR01083; EGYSTEROIDR.

PRINTS; PR01083; EGYSTEROIDR.

PRINTS; PR00039; STRDHORMONE.

PRINTS; PR00043; STRDHORMONE.

R PRINTS; PR000430; Znf C4steroid; 1.

R PARRYT; SM00430; Znf C4steroid; 1.
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DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 441 AA; 50229 MW; AF7FD8E8F11741CB CRC64;
                            Xenopus research: The NIH Xenopus
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Richardson P.; "Genetic and genomic tools for
                                                                     Dev. Dyn. 225:384-391(2002)
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EMBL; BC092160; AAH92160.1; -; mRNA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003707; F:steroid hormone receptor activity; IEA.
GO; GO:0004887; F:thyroid hormone receptor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
SEQUENCE 412 AA; 47679 MW; 30E5C4BBCDIAC86D CRC64;
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---AlaArgThrSerThrValAlaThrProSerProAlaPro-----
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Q9Z0Y9; Q9QUH7;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Oxysterols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1283; ECDYSTEROIDR.
PRINTS; PRO0398; STRODPGRWONER.
PRINTS; PRO00045; STROIDFINGER.
PRODOM; PD000031; NUCLEAR REC DBD 1; 1.
PROSITE; PS010031; NUCLEAR REC DBD 2; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ; TISSUE=Liver;
MEDLINE=20156373; PubMed=10675617; DOI=10.1016/S0378-1119(99)00555-7;
Alberti S., Steffensen K.R., Gustafsson J.-A.;
"Structural characterisation of the mouse nuclear oxysterol receptor genes LXRalpha and LXRbeta.";
Gene 243:93-103(2000).
                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 nuclear receptor DNA-binding domain.
                                                                                                                 receptor LXR-alpha).
Name=Nrlh3; Synonyms=Lxra;
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                                                                                                                                                                                             :::||| |||
-----ArgValSerSerProProGlnValLeuPro-----
I; Zinc; Zinc-finger.

Nuclear receptor.

NR C4-type.

NR C4-type.

Ligand-binding (Potential).

R > P (in Ref. 2)

7 MW; CC9A8DF38D935593 CRC64;
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1152
335
24
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                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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96 116
132 156
213 432
399 399
445 AA; 50477 M
 Transcription regulation;
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Search completed: November 25, 2005, 22:30:18 Job time : 231 secs



8058, Ap 8413, Ap 8, Appli 8, Appli 1, Appli 2, Appli 2, Appli 2, Appli 14, Appl 78, Appl 11, Appl 72, Appl 10, Appl 10, Appl 105, Appl 105, Appl 2, Appl

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| Patent No. 5607967
| GENERAL INFORMATION:
| APPLICANT: Friedman, Bitan
| APPLICANT: Friedman, M. Katharine
| APPLICANT: Schaidt, Azriel
| APPLICANT: Schaidt, Azriel
| TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
| UNMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,518
FILING DATE:
                       US-00-342-411A-4
US-00-342-411A-4
US-00-342-411A-4
US-00-949-016-8413
US-08-463-694-8
US-08-694-501-8
US-08-694-501-8
US-08-66-2
US-10-329-668-2
US-10-329-668-2
US-10-087-167-82
US-10-087-167-82
US-10-087-167-88
US-10-087-167-88
US-10-087-167-14
US-10-087-167-18
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NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
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STATE: New Jersey
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    Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cgn2_1/USFTO_spool_p/US10712629/runat_25112005_143037_11014/app_query.fasta_1.903
-Q=/Cgn2_1/USFTO_spool_p/US10712629/runat_25112005_143037_11014/app_query.fasta_1.903
-D=Lssued_PatenTes AA -QFWR=fastan -SUPFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MINE-0 -ALRANS=human40.cdi
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10712629 @CGN 1 1 71 @runat_25112005_143037_11014 -NCPU=6 -ICPU=3
-NO NMAP -LARGEQUERY -NGE_SCORES=0 -MAXT -DSPBALOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADEL -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2, Appli
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Sequence 7717, Ap
Sequence 655, Appli
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                       - protein search, using frame_plus_n2p model
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US-08-646-248-2
PCT-US95-13924-2
PCT-US95-13931-2
US-09-949-016-7717
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US-10-329-668-4
US-08-776-844-2
US-09-909-325-2
US-09-909-326-2
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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No.
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ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
US-08-330-283-2; Sequence 2, Application US/08330283; Patent No. 5679518; GENERAL INFORMATION:
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Matches:
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Mismatches:
Indels:
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LENGTH: 461 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-330-518-2
                                                                                      1.1e-104
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241 GICACGCCCIGGCCCCTGGGCGCAGACCCCCAGICCCCGAGAIGCCCGCCAGCAACGCIII 300 1 AAGATTCGGAAACAGCAGCAGCAGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 461 248 0 1 1 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-712-629B-2 (1-746) x US-08-330-283-2 (1-461)

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289 ValProGlyPheLeuGlnLeuGlyArgGluAspGlnIleAlaLeuLeuLysAlaSerThr 308
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  TELEFAX: (908) 594-4720
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                          1.1e-104
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REGENERAL INFORMATION:

APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Holloway, M. Katharine
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
ITTLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STREET: 126 East Lincoln Avenue
CITY: Rahway
STREET: US
CONTRY: US
CONTRY: US
CONTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatibl
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REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19327
TELECOMMUNICATION:
TELEPHONE: (908) 594-4283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,283
FILING DATE: 27-02F-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 5939322
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               249 ValThrProTrpProLeuGlyAlaAspProGlnSerArgAspAlaArgGlnGlnArgPhe
                                                                     301 GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA
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GTCACGCCCTGGCCCTGGGCGCAGACCCCCAGTCCCGAGATGCCCCCCCAGCAACGCTTT
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STATE: New Jersey
COUNTRY: New Jersey
COUNTRY: New Jersey
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/13931
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 ATCAAGAGGCCGCAGGACCAGCTGCGC 746
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NAME: QUAGAILEC, GATOL S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19316 PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 antino acids
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                                                Squence 2, Application PC/TUS9513924

GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rulledge, Su Jane
APPLICANT: Schmidt, Azriel
APPLICANT: Schmidt, Azriel
APPLICANT: Schwidt, Azriel
APPLICANT: Schwidt, Azriel
APPLICANT: Schwidt, Sariel
APPLICANT: MURBEN OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    STREET: 140 Gast CITY: Rahway
STATE: Naw Jersey
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13924
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAMME: OUGGIlato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19327 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
INFORMATION: (908) 594-4720
INFORMATION: SEQUENCE CHARACTERISTICS:
LENGTH: 461 emino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
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Matches:
Conservative:
Mismatches:
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STREET: 126 East Lincoln Avenue
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Best Local Similarity:
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                       RESULT 4
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                                           461
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                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                           US-10-712-629B-2 (1-746) x PCT-US95-13931-2 (1-461)
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                                                                   Gaps:
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1231.00
99.60$
99.60$
TYPE: amino acid
STRANDEDRES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTL-SENSE: NO
PCT-US95-13931-2
                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                      Alignment Scores:
Pred. No.:
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5-09-949-016-7717 Sequence 7717, Application US/09949016

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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOM, 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 717
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Matches:
Conservative:
Mismatches:
Indels:
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1231.00
99.60%
99.50%
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Human
US-09-949-016-7717
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity:
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                                                                                                    Sequence 655, Application US/09976594

Sequence 655, Application US/09976594

Sequence 655, Application US/09976594

Sequence 655, Application US/09976594

GENERAL INFORMATION:
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
TILE OF INVENTION: GENES
FILE REFERENCE: PA-0041 US
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT APPLICATION NUMBER: 600240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ 1D NOS: 1143

SOCTWARE: PERL PROGRAM

SEQ 1D NO 655

LENGTH: 461
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                          461
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; OTHER INFORMATION: Incyte ID No. 6673549 3721108CD1
US-09-976-594-655
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Matches:
Conservative:
Mismatches:
Indels:
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1227.00
99.20%
99.20%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-976-594-655
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-776-844-2
US-08-776-844
; Patent No. 6277976
; GENBRAL INFORMATION:
APPLICANT: BNARK, EVA
APPLICANT: GUSTAFSSON, JAN
                                          2.9e-103
1215.50
99.20%
99.20%
88.46%
            Homo Sapien
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                      Alignment Scores:
Pred. No.:
   ; TYPE: PRT
; ORGANISM: HC
US-10-329-668-4
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                                                                                                                               CAGCAGTTGGTGGCGGCCCAACTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAA
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; Patent No. 6696473
; GENERAL INFORMATION:
; APPLICANT: Martin Richard
; APPLICANT: Brenton Todd
; APPLICANT: Kahl Jeffrey Dean
; APPLICANT: Kahl Jeffrey Dean
; APPLICANT: Wang Tie-Lin
; TITLE OF INVENTION: HETEROCYCLIC MODULATORS OF NUCLEAR RECEPTORS
; FILE REFERENCE: 38205-3001
; CURRENT APPLICATION NUMBER: US/10/329, 668
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
US-10-712-629B-2 (1-746) x US-08-342-411A-2 (1-460)
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US-10-329-668-4
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274 ValProGlyPheLeuGlnLeuGlyArgGluAspGlnIleAlaLeuLvBAlaSerThr 293
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                                                                                                  ATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAELEEQ for Windows Version 2.0
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: -CUNKNOWN>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/909,325
FLING DATE: 19-Jul-2001
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                    720 ATCAAGAGGCGCAGGACCAGCTGCGC 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09909325
Patent No. 6525188
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-508-9100
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GUSTAFSSON, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-508-9299
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
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Matches:
Conservative:
Mismatches:
Indels:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,844
FILING DATE: 24-JUN-1997
CLASSIFCATION NATA:
APPLICATION NUMBER: PCT/EP95/03247
FILING DATE: 16-AUG-1995
APPLICATION NUMBER: UK 9413536.2
APPLICATION NUMBER: UK 9413536.2
APPLICATION NUMBER: 32141
REGISTRATION NUMBER: 32141
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION:
TELEPHONE: 202-508-9190
      RECEPTOR
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-712-629B-2 (1-746) x US-08-776-844-2 (1-446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
   TITLE OF INVENTION: OR-1 ON ORPHAN RETITLE OF INVENTION: TO THE NUCLEAR RENUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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1101.00
92.77$
90.36$
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LENGTH: 446 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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STRANDEDNESS: si
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| ProSerArgValGluAlaLeuGlnGlnProTyrValGluAlaLeuLeuSerTyrThrArg 393
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                                                                   446
225
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112
7
                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                    US-10-712-629B-2 (1-746) x US-09-909-325-2 (1-446)
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
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US-09-300-326-2
; Sequence 2, Application US/09909326
; Patent No. 6617120
; GENERAL INFORMATION:
                                                                 9.39e-93
1101.00
92.77%
90.36%
80.13%
                                                                                   Percent Similarity:
Best Local Similarity:
                                                          Alignment Scores:
                                       US-09-909-325-2
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1 AAGATTCGGAAACAGCAGCAGCAGGAGTCACAGTCACAGTCGCAGTCACCTGTGGGGCCG 60
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225
6
112
1
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FILING DATE: 19-Jul-2001
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: 19-70-66-24
APPLICATION NUMBER: 08/776,844
APPLICATION NUMBER: 08/776,844
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR
TO THE NUCLEAR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-712-629B-2 (1-746) x US-09-909-326-2 (1-446)
                                                  NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-09-909-326-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                   ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
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1101.00
92.77#
90.36#
80.13#
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Best Local Similarity:
                                                                                                                                                        COUNTRY:
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Length: Matches: Conservative: Mismatches: Indels:

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3e-92
1095.50
93.57%
89.56%
79.73%
protein
                                                                                                Percent Similarity:
Best Local Similarity:
MOLECULE TYPE:
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                                                 Alignment Scores
   ; MOLECULE T)
JS-08-372-652-3
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J. Sequence 3, Application US/08372652

J. Sequence 3. Application US/08372652

J. Patent No. 5932699

J. TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING

J. TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING

J. TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS

J. CORRESPONDERS: J. POLYPERS: J. SEQUENCES: J. T. CORRESPONDERS: J. SECONDERS: J. J. SE
                                                                                  GCCCACTTCACGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA
                                     AlaHisPheThrGluLeuAlaIleIleSerValGluGluIleValAspPheAlaLysGlu
                                                                                                                                                       ATCGAGATCATGCTGCTAGAGACAGCCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
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STRANDEDNESS: not relevant
TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hueng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
446
223
10
15
2
                                                                                                      US-10-712-629B-2 (1-746) x US-08-372-652-3 (1-446)
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                                                                          Gaps:
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660 CCGGGCCGCTGGAGGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGTCCTACACGCGC 719
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                                                                                                                                                                                               PhelleAsnProllePheGluPheSerArgAlaMetArgArgLeuGlyLeuAspAspAla 353
                                                                                                                                                                                                                                  GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG 659
                                                                                                                                                                                                                                                                                                                   274 ValProGlyPheLeuGlnLeuGlyArgGluAspGlnIleAlaLeuLeuLysAlaSerThr 293
                                                     ATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
                                                                                                  TTCTTGAG-GACTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCCTGCAGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSER: A ALOLIG, White & Durkee
STREET: P.O. Box 4433
CITY: Houseon
STATE: TX
COUNTRY: USA
ZITY: HOUSEON
STATE: TX
COUNTRY: USA
ZITY: T7210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,411A
FILING DATE: IB-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 31,928
RELERBANCE/DOCKET NUMBER: ARCD154
TELEBRAK: (512) 418-3000
TELEBRAK: (512) 418-3000
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APPLICANT: SONG, Ching
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
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Matches:
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TELER: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TWATH: 443 amino acids
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FITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
        NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCES: 17
CITY: 225 Franklin Street, Suite 3100
CITY: 225 Franklin Street, Suite 3100
STATE: MA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: 160ppy disk
COMPUTER: 1BM FC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
OFFRAHE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE: 10-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 00/302,652
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 00/36/246001
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-5070
TELEFEX: 200154
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Indels:
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STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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           ATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACCACGAGACAGAGTGTATCACC
US-10-712-629B-2 (1-746) x US-08-342-411A-4 (1-443)
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Search completed: November 25, 2005, 22:33:18 Job time: 46 secs

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Publication No. US20020116731A1

GENERAL INPORMATION:
APPLICANT: Guenther, Catherine
APPLICANT: Allen, Keith D.
APPLICANT: Allen, Keith D.
APPLICANT: Baribault, Helene
ITILE OF INVENTION: TRANSGENIC MICE CONTAINING RETINOID X
ITILE OF INVENTION: RECEPTOR INTERACTING PROTEIN GENE DISRUPTIONS
FILE REPERENCE: R-684
CURRENT APPLICATION NUMBER: US/10/013,823
CURRENT APPLICATION NUMBER: US 60/254,801
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 5
CONTAIN CONTAIN NUMBER: US 60/309,404
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5 US-10-899-458-10

6 US-10-899-458-8

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1 US-10-329-458-6

1 US-10-921-023-2

1 US-10-921-023-4

1 US-10-921-023-2

1 US-10-921-023-2
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Matches:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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US-10-013-823-3
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        Sequence 3, Appli
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-418-007-4
US-10-899-458-12
US-10-500-912-4
US-10-327-813-4
US-10-717-049-4
US-10-509-197-4
US-09-909-446-2
US-09-909-446-2
US-09-909-325-2
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Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Perfect score:
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                                       Length:
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                                    7.69e-88
1231.00
99.60%
89.59%
    TYPE: PRT

ORGANISM: Homo sapiens
US-10-418-007-4
                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                 Alignment Scores
Pred. No.:
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; Sequence 4, Application US/10418007
; Publication No. US20040018560A1
; GENERAL INPORMATION:
; APPLICANT: Miller, Ann B.
; APPLICANT: Moore, John
; APPLICANT: Williams, Shawn P.
; APPLICANT: Willely, George B.
; TITLE OF INVENTION: CRYSTALLIZED LXR POLYPEPTIDE IN COMPLEX WITH A LIGAND AND SCREE; TITLE OF INVENTION: METHODS EMPLOYING SAME; TITLE OF INVENTION: METHODS EMPLOYING SAME; FILE REFERENCE: PU4691
; CURRENT APPLICATION NUMBER: US/10/418,007
; CURRENT APPLICATION NUMBER: US/10/418,007
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
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Sequence 4, Application US/10500912
Publication No. US20050123580A1
GENERAL INFORMATION:
APPLICANT: BULTIS, Thomas P.
TITLE OF INVENTION: Method of Treating Atherosclerosis and Hypercholesterolemia
FILE REFERENCE: X-14934
CURRENT APPLICATION NUMBER: US/10/500,912
CURRENT FILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.3
                                                           228
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CRGANISM: homo sapiens
US-10-500-912-4
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       APPLICANT: Lu, Shao-po

APPLICANT: Mohan, Raju

APPLICANT: Schweiger, Edwin J.

APPLICANT: Schweiger, Edwin J.

APPLICANT: Schweiger, William C. Jr.

APPLICANT: Stevens, William C. Jr.

APPLICANT: Xie, Yinong

TITLE OF INVENTION: MODULATORS OF LXR

FILE REFERENCE: 98049.4161.

CURRENT FILING DATE: 2004-07-24

PRIOR APPLICATION NUMBER: US 10/327,813

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: US 60/342,707

PRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 12

LENGTH: 461

TYPE: PRT

TYPE: PRT

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TYPE: PRT
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99.60$
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Johnson, Alan T
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ORGANISM: Homo Sapien
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Sequence 4, Application US/10327813

Publication No. US20030181420A1

GENERAL INFORMATION:

APPLICANT: Bayne Christopher D.

APPLICANT: Lu Shaco Po

APPLICANT: Lu Shaco Po

APPLICANT: Mohan Raju

CURRENT APPLICATION NUMBER: US/10/327,813

CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 60/342,707

PRIOR APPLICATION NUMBER: 60/342,707
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US-10-327-813-4
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                   Conservative:
Mismatches:
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US-10-509-197-4

Sequence 4, Application US/10509197

Publication No. US20050171084A1

GENERAL INFORMATION:
APPLICANT: Burbidge, Stephen A.
APPLICANT: Cairns, William J.
APPLICANT: Irving, Elaine A.
APPLICANT: Richardson, Jill C.
APPLICANT: Soden, Peter E.
APPLICANT: Vinson, Mary
APPLICANT: Winson, Mary
APPLICANT: Winson, Mary
APPLICANT: Whitney, Karl D.
                  99.20%
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rercent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Flatt Brenton Todd
APPLICANT: Flatt Brenton Todd
APPLICANT: Kahl Jeffrey Dean
APPLICANT: Kahl Jeffrey Dean
APPLICANT: Wang Tie-Lin
TITLE OF INVENTION: HETEROCYCLIC MODULATORS OF NUCLEAR RECEPTORS
FILE REFERENCE: 38205-3001B
CURRENT APPLICATION NUMBER: US/10/717,049
FRIOR APPLICATION NUMBER: 10/329,668
PRIOR PILING DATE: 2002-12-20
PRIOR PILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No.:
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US-09-925-297-635
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Matches:
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Mismatches:
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  with
FILE OF INVENTION: Methods of Treatment with FILE REFERENCE: P51332
CURRENT APPLICATION NUMBER: US/10/509,197; CURRENT FILING DATE: 2004.09-24; PRIOR APPLICATION NUMBER: PCT/US03/09225; PRIOR FILING DATE: 2003-03-26; PRIOR FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 460
                                                                                                                                                                         1.26e-86
1215.50
99.20%
89.20%
                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-509-197-4
                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: +UDIKNOWN-
FILING DATE: +UDIKNOWN-
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SEQUENCE DESCRIPTION: SEQ ID
US-09-909-446-2
                                                                                                                                                                                                                           LENGTH: 446 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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1101.00
92.77%
90.36%
80.13%
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Best Local Similarity:
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-G1ySerSerSerSerAlaSerG1yProG1yAlaSerProG1yG1yG1yBe
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FAMILY
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
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APPLICATION NUMBER: US/09/909,446
FILING DATE: 19-5ul-2001
CLASSIFICATION: <a href="https://doi.org/10.10m/">doi.org/</a>
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APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN I
TO THE NUCLEAR
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ADDRESSE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09909446
Patent No. US20020052489Al
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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US-09-909-446-2
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                                                                                            AGCCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAACAGCGGCTCAAGAACTAATGATC
                                                                                                                                                       CAGCAGTIGGIGGCGCCCAACTGCAGTGCAACAAAACGCTCCTTCTCCGACCAGCCCAAA
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 ATCAAGAGGCCGCAGGACCAGCTGCGC 746
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160 LysIleGlnLysGlnGlnGlnGln--
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Patent No. US20020128461A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wi
STREET: 1001 G Street,
CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ENMARK, EVA
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   GAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAG
                                                                 CCGGGCCGCGTGGAGGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGTCCTACACGCGC
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GUSTAFSSON, JAN
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,325
FILING DATE: 19-Jul-2001
CLASSIFICATION ADATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
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Mismatches:
Indels:
Gaps:
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REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-712-629B-2 (1-746) x US-09-909-325-2 (1-446)
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Matches:
                                                                                                                              720 ATCAAGAGGCCGCAGGACCAGCTGCGC 746
                                                                                                                                                NO: 2:
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
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SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acida
TYPE: amino acid
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Patent No. US20020115847A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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1101.00
92.77%
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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   CCGGGCCGCGTGGAGGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGTCCTACACGCGC
                                                                                                                                                                                                                                          Sequence 2, Application US/10013823
; Sequence 2, Application US/10013823
; Publication No. US20202016731A1
; Publication No. US20202016731A1
; GENERAL INFORMATION:
; APPLICANT: Guenther, Catherine
; APPLICANT: Allah, Keith D.
; APPLICANT: Zhang, Qin
; APPLICANT: Zhang, Qin
; APPLICANT: Allah, Keith D.
; APPLICANT: Bribault, Helene
; TITLE OF INVENTION: TRANSGBUI MICE CONTAINING RETINOID X
; TITLE OF INVENTION: RECEPTOR INTERACTING PROTEIN GENE DISRUPTIONS
; TITLE OF INVENTION: RECEPTOR INTERACTING PROTEIN GENE DISRUPTIONS
; TITLE OF INVENTION: RECEPTOR INTERACTING PROTEIN GENE DISRUPTIONS
; TITLE OF INVENTION NUMBER: US 60/254,801
; PRIOR PEPLICATION NUMBER: US 60/254,801
; PRIOR PEPLICATION NUMBER: US 60/309,404
; PRIOR APPLICATION NUMBER: US 60/309,404
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FRASER FOR FOR Windows Version 4.0
; IRNATH: AND 2.
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Best Local Similarity:
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TYPE: PRT
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Matches:
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Indels:
Gaps:
                                                         APPLICATION NUMBER: 08/776,844
FILING DATE: 1997-06-24
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGBAN, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-712-629B-2 (1-746) x US-09-909-326-2 (1-446)
APPLICATION NUMBER: US/09/909,326
FILING DATE: 19-Jul-2001
CLASSIFICATION: 435
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-09-909-126-2
                                                                                                                                                                                                                                                                                 LENGTH: 446 amino acids
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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92.77%
90.36%
                                                PRIOR APPLICATION DATA:
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Best Local Similarity:
Query Match:
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174 GluproAlaAlaSerSerSerGlyArgProAlaAlaSerProGlyThrSerGluAlaSer 193
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Sequence 8, Application US/10899458

Publication No. US20050080111A1

GENERAL INFORMATION:
APPLICANT: Bayne, Christopher D.
APPLICANT: Johnson, Alan T.
APPLICANT: Mohan, Raju
APPLICANT: Mohan, Raju
APPLICANT: Schweiger, Edwin J.
APPLICANT: Schweiger, Edwin J.
APPLICANT: Schweiger, Edwin J.
APPLICANT: Stevens, William C. Jr.
APPLICANT: Wang, Haixia
APPLICANT: Stevens, William C. Jr.
APPLICANT: WHOREN: US/10/899,458
CURRENT FILING DATE: 2004-07-24
PRIOR APPLICATION NUMBER: US 60/342,707
PRIOR PRIDR PRIOR DATE: 2001-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 ATCAAGAGGCGCAGGACCAGCTGCGC 746
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Publication No. US20050080111A1
GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-10-899-458-10
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NUMBER OF SEQ ID NOS: 27

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                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                       4.17e-77
1094.00
92.37%
89.96%
         LENGTH: 443
TYPE: PRT
CORGANISM: Rattus norvegicus
US-10-899-458-8
                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                   Alignment Scores
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Search completed: November 25, 2005, 22:38:27 Job time : 161 secs



November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbm (Published_Applications_NA_New).
.rapbm (Published_Applications_AA_Main) and .rapbm (Published_Applications_AA_New).



Run on:

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Sequence 4, Application US/10519447

Sequence 4, Application US/10519447

Publication No. US20050244829A1

GENERAL INFORMATION:

APPLICANT: Makoto OGINO

APPLICANT: Hideki ENDOH

TITLE OF INVENTION: METHOD FOR SCREENING AN ACENT FOR IMPROVING INSULIN RESISTANCE

FILE REFERENCE: Q85576

CURRENT APPLICATION NUMBER: US/10/519,447

CURRENT APPLICATION NUMBER: DCT/JP03/08367

PRIOR APPLICATION NUMBER: DCT/JP03/08367

PRIOR APPLICATION NUMBER: JP 2002-193814

PRIOR FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 4
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4, Appli
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US-10-712-629B-2 (1-746) x US-10-519-447-4 (1-505)
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174.50
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12.70%
 TYPE: PRT
ORGANISM: Homo sapiens
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-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-C=Cgn2 1/USF70 spool p/US10712629/runat_25112005 143038_11026/app_query.fasta_1.903
-DS=Published Applications AA New -OFMT=fastan -SUFFTX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=E0
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR CORPERS=CCt -THR MAX=E0
-MAXLEN=200000000 -USER=S10712629 @CGN 1 1 1 @runat 25112005 143038 11026
-NCPU-$C -ICPU=3 NO MMAP -LARGEQUERY NEG SCORES=0 -MATR -DSPBICK=100
-LONG:29G -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1096, Ap
Sequence 1641, Appl
Sequence 1431, Ap
Sequence 44, Appl
Sequence 964, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 41, Appl
                                                                                                                                           (without alignments)
1004.935 Million cell updates/sec
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1374
1 aagattcggaaacagcagca......ggccgcaggaccagctgcgc 746
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1: /cgn2_6/ptodata/2/pubpas/US10 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpas/US07 NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpas/US07 NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpas/US07 NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpas/US08 NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpas/US08 NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpas/US1 NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpas/US1 NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US1 NEW PUB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                - protein search, using frame plus n2p model
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US-110-821-234-1096
US-11-015-546-20
US-10-821-234-1641
US-11-053-100-44
US-11-053-100-48
US-11-053-100-49
US-11-053-100-49
US-11-059-982-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Result

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477 GluProGlyProThrGlyLeuProGlyProProGlyGluArgGlyGlyArgGlySerArg 496
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TCTGAGGCAGCAG------CCAGGGCTCCGGGGAAGGCGAGGGTGTCCAGCTAAC 158
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322 AlaGlyAlaArgGlyAsnAspGlyAlaThrGlyAlaAlaGlyProProGlyProThrGly 341
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| GlyProArgGlySerGluGlyProGlnGlyValArgGlyGluProGlyProGlyPro 381
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                                                                                                                                                                                          342 ProAlaGlyProProGlyPheProGlyAlaValGlyAlaLysGlyGluAlaGlyProGln 361
                    611 GCTCATCGCCATCAACATCTTCTCGGCCGACCGGCCCAACGTGCAGGAGCCGGGCCGCGT
                                                                                                                                                                                                                                233 AGCCCAAAGTCACGCCCTGGCCCTGGCG-----CAGACCCCCAGTCCCGAGATGCCC
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APPLICANT: FOX, BRIAN A.
APPLICANT: HOLLOWAY, JAMES L.
APPLICANT: HOLLOWAY, JAMES L.
APPLICANT: APPLESY, MARK
TITLE OF INVENTION: ZLNÉ13, A TUMOR NECROSIS FAC
FILE SPERENCE: 03-24
CURRENT APPLICATION NUMBER: US/11/015,546A
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 60/530,185
PRIOR FILING DATE: 2003-12-16
SROW FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 GCGCATCAAGAGGCCGCAGGACCAGCT
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APPLICANT: SHEPPARD, PAUL O.
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285 ProAlaGlyProLygGlyGluProGlySer-----ProGlyGluAsnGlyAlaPro 301
                                                                                                     311 GlnGlyCysGlnPheArgSerValGluAlaValGlnGluIleThrGluTyrAlaLysSer 330
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331 IleProGlyPheValAsnLeuAspLeuAsnAspGlnValThrLeuLeuLysTyrGlyVal 350
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nLysAspGlyValLeuIleSerGluGlyGlnGlyPheMetThrArgGluPheLeuLysSe 383
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Aradamani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: MADBER: US/10/821,234
CURRENT APPLICATION NUMBER: US/60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SEQ ID NO 1096
LENGTH: 1467
                          :::||| ||| |||
291 LysPheLysHisIleThrProLeuGlnGluGlnSerLysGluValAlaIleArgllePhe
                                                                                 -------GCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAGCAA
                                                                                                                                                         361 GIGCCIGGITICCIGCAGCIGGGCCGGGAGCACCAGAICGCCCICCIGAAGGCAICCACI
                                                                                                                                                                                                                                                                             351 HisGluIleIle-----------Tyr-ThrMetLeuAlaSerLeuMetAs
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443 lnAlaLeuGluLeuGlnLeuLysLeuAsnHisProGlu 455
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US-10-821-234-1096
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Best Local Similarity:
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408 GluProAlaArgProArgAlaGlyAlaProArgThrArgGlyGlnSerGlyArgGluPro 427
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                                                                                                                                                                                                                                                                                                                                                    237 CAAAGTCACGCCCTGGCCCCTGGGCGCAGACCCCCAGTCCCCGAGATGCCCG---CCAGCA
                                                                                                                                                                                                                                                                                                                                                                     503 ArgGlyAlaHisGlyHisAlaArgPro--LeuProGlnAspArgHisAlaLeuProGluS
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                               sequence, polypeptide sequence fusion
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78
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51
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Matches:
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial DNA
OTHER INFORMATION: the MBP-ztnf13
                                                                                   0.015
117.50
38.11%
31.97%
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Best Local Similarity:
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US-10-821-234-1641
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Sequence 1641, Application US/10821234 Publication No. US20050255114A1

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1525 ThrProAlaTyrGlyAlaTrpSerProSerValGlySerGlyMetThrProGlyAlaAla 1544
             APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 81A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PLING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1641
LENGTH: 1970

"WITH DATE: 1970
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|1616 erProThrSerProSerTyrSer-----ProThrSerProSerTyrSerProThrSerP 1634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 CCAGATCGCCCTCCTGAAGGCATCCACTATCGAGATCATGCTGCTAGAGACAGCCAGGCG 452
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Mismatches:
Indels:
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Matches:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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Best Local Similarity:
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Pred. No.:
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Oy 442 ACAGCCAGGCCTACAACCACGAGACGAGAGTATACACCTTCTTGAGGACTTCACCTACA 501 ::: bb 622 yGluProGlyvalvalGlyAlavalGlyThrAlaGlyProSer	PRIOR PAPLICATION NUMBER: US 09/812,382 PRIOR FILING DATE: 2001-03-20 PRIOR FILING DATE: 2000-03-20 PRIOR FILING DATE: 2000-03-20 NUMBER OF SEQ ID NOS: 58 SOFTWARE: Patentin version 3.3 SEQ ID NO 44 LENGTH: 735 TYPE: PRT ORGANISM: Artificial FEATURE: OTHER INFORMATION: Synthetic Construct FEATURE: NAME/KEY: MISC_FEATURE COCATION: (1)(735) OTHER INFORMATION: pet15b-SD3-ELP1-90-throm-Small Heterodimer partner orphan COTHER INFORMATION: receptor	US-11-053-100-44 Alignment Scores: 0.0322 Length: 735 Pred. No.: 113.00 Matches: 84 Score: 317.63\$ Conservative: 24 Best Local Similarity: 29.27\$ Indens: 83 Query Match: 7 Gaps: 16 DB: 7 Gaps: 16	x us-il-uss-inu-44 (i 4GGGCAGCAGCAGCTCAGCCTC [
0y 620 CATCAACATCTTCTCGCCCGACGGCCCAACGTGCAGGCCGGG 664	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: 116.50 Matches: 76 Percent Similarity: 34.50\$ Conservative: 13 Best Local Similarity: 29.46\$ Mismatches: 102 Query Match: 1 Gaps: 13 US-10-712-629B-2 (1-746) x US-10-821-234-1431 (1-1366) Qy 49 CCTGTGGGGCGCAGGGCAGCAGCAGCAGCAGCAGGCAGCAGGCAGCA	499 Ġİ'PE'OThrGlyAspE'rÖĞİ'YASBENĞİ'YASDİYSGIYHiSAlaĞİ'YE'UAlaĞİ'YA 139 GGCGGGGTGTCCAGCTAACAGGGCTCAAGAACTAATGATCAGCAGTTGGTGGCG	Qy 256 CTGGGCGCAGACCCCGAGATGCCGGCAACGCTTTGCCCACTTCACG 312 Db 552 rodlyPhedinGlyLeuProGlyProSerGlyPro

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Best Local Similarity: 27.38* Mismatches: 49 Query Match: 8.15* Indels: 60 DB: 1 Gaps: 7 US-10-712-629B-2 (1-746) x US-10-821-234-964 (1-1166)	Oy 43 CAGTCACCTGTGGGGCCGCAGGGCAGCAGCACCTCAGCCTCTGGGGCTTCCCCT 102	Qy 103 GGTGGATCTGAGGCAGCGCAGCGCGGGAAGGCGAGGGTGTCCAGCTAAC 158	Qy 159 182 	Qy 183	Qy 202 CTGCAGTGCAACAAACGCTCCTTCTCCGACCAGCCCAAAGTCACGCCCTGGCCCCTGGGC 261 Db 179 laGly 180	Qy 262 GCAGACCCCCAGTCCCGAGATGCCCGCCAGCACTTTGCCCACTTCACGGAGCTGGC 321	Oy 322 ATCATCTCAGAGATCGTGGACTTCGCTAAGCAAGTGCCTGGTTTCCTGCAGCTG 381	Qy 382 GGCCGGAGACCAGATCGCCCTCCTGAAGGCATCCACTATCGAGATCATGCTGCTAGAG 441	Qy 442 ACAGCCAGGCGCTACAACCA 461 I ::::::::::::::::::::::::::::::::::::	RESULT 8 US-11-053-100-48 US-11-053-100-48 Sequence 48, Application US/11053100 Publication No. US2005025554A1 GENERAL INFORMATION: FILE REPERENCE: 4176-101 CIP CURRENT CHILKOTON CURRENT FILING DATE: 2005-02-08 PRIOR APPLICATION NUMBER: US/11/053,100 PRIOR PRIOR PLICATION NUMBER: US/9/812,382 PRIOR PAPPLICATION NUMBER: US/9/812,382 PRIOR PRIOR PLILING DATE: 2000-03-20 PRIOR PRIOR PLILING DATE: 2000-03-20 PRIOR PRIOR FILING DATE: 2000-03-20 NUMBER OF SEQ ID NOS: 58 SEQ ID NO 48 LENGTH: 624 TYPE: PRT ORGANISM: Artificial FEATURE: CTHER INFORMATION: Synthetic Construct FEATURE: COTHER INFORMATION: Synthetic Construct FEATURE: COTHER INFORMATION: PETISD-SD3-ELPI-60-throm-Estrogen receptor ligand binding domain Alignment Scores: Alignment Sc
Db 490GlnGlyAlaAlaSerArgProAlaIleLeuTyrAlaLeuLeuSerSerSerLeuLys 508 Qy 270 CCAGTCCCGAGATGCCCGCCAGCAACGCTTTGCCCACTTCACGA	Qy 315 GCTGGCCATCATCTCAGAGATCGTGGACTTCGC 353	Qy 354 TAAGCAAGTGCCTGGTTTCCTGCAGCTGGGCCGGAAGACCAGATCGCCCTCCTGAAG 411	Qy 412	Qy 430	Qy 459 CCACGAGACAGAGTGTATCACCTTCTTGAGGACTTCACCTACAGGACGACTTCCA-517	Oy 518CCGTGCAGGCCTGCAGGTGGAGTTCATCAACCCCATCTTCGAGTTCTCG 566	Qy 567 CGGGCCATGCGGCGGCTGGACGACGCTGAGTACGCCCTGCTCATCGCCATCAAC 626 1::	Qy 627 ATCTTCTCGGCCGACGGCCCAACGTGCAGGAGCCGGGCGTGGAGGCGTTGCACAG 686 :::	Qy 687CCCTACGTGGAGGGGTGGTGTCCTACACGCGCATCAAG 725 	Oy 726 AGGCCGAGGACC 738 Db (89 nGlyArgLeuThr 693) RESULT 7 US-10-81-234-964 ; Sequence 964, Application US/10821234 ; Sequence 964, Application US/10821234 ; Sequence 964, Application US/0821234 ; Sequence 964, Application US/10821234 ; Publication No. US20050255114A1 ; Publication No. US20050255114A1 ; Publication No. US20050255114A1 ; APPLICANT: Labat, Ivan ; APPLICANT: Andarmani, Susan ; APPLICANT: Andarmani, Susan ; APPLICANT: Andarmani, Susan ; APPLICANT: Tang, Y. Ton ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia ; TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia ; CURRENT APPLICATION NUMBER: US/10/821,234 ; CURRENT APPLICATION NUMBER: US 60/462,047 ; PRIOR FILING DATE: 2004-04-07 ; NUMBER OF SEQ ID NOS: 1704 ; SCOTTARE: pt SEQ_genes Version 1.0 ; SCOTTARE: PRT ; ORGANISM: Homo sapiens US-10-821-234-964 Alignment Scores: 0.0378 Length: 1166 SCOTTARE: PT PRT SCOTTARE: PT PRT ALTON PRIOR PT PRT SCOTTARE: PT PT PRT SCOTTARE: PT PT PT PT PT PT PT PT PT PT PT PT PT

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474 ProArgGlySerHisMetSerLysLysAsnSerLeuAlaLeuSerLeuThrAlaAspGln 493
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545 GlyPheValAspLeuThrLeuHisAspGlnValHisLeuLeuGluCysAlaTrpLeuGlu 564
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                                                                         GTGGGGCCGCAGGCAGCAGCTCAGCCTCTGGG----CCTGGGGCTTCC---CCTGGT
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; Sequence 1, Application US/11059982
; Publication Vo. US20050255507A1
; Publication Vo. US20050255507A1
; Publication No. US20050255507A1
; APPLICANT: Jenkine, Robert B. APPLICANT: Thibodeau, Steve
; APPLICANT: Thibodeau, Steve
; APPLICANT: Wang, Liang
; TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
; TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
; TITLE OF INVENTION: PROGNOSIS OF PROLIFERATIVE DISORDERS
; TIER REFERENCE: 07039-505001
; CURRENT APPLICATION NUMBER: US 60/545,573
; PRIOR APPLICATION NUMBER: US 60/545,573
; PRIOR APPLICATION NUMBER: US 60/545,573
; PRIOR FILING DATE: 2005-02-17
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NOS: 50
; SEQ ID NOS: 50
; LENGTHUM OF THE TENGENCE OF WINDOWS VERSION 4.0
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                                US-10-712-629B-2 (1-746) x US-11-053-100-49 (1-774)
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-982-1
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OTHER INFORMATION: pET15b-SD5-ELP1-90-throm-Estrogen receptor ligand binding domain
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                                                                                                                                                                                                                                                                                                                                   324 ProArgGlySerHisMetSerLysLysAsnSerLeuAlaLeuSerLeuThrAlaAspGln 343
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                                                                                                                                                                                                                      106 GGATCTGAGGCAGCCAGCCAGGGCTCCGGGGAAGGCGAGGGT--------
                                                                                                                                                                                                                                                           304 GlyGlyValProGlyTrpProSerSerGlyGlyGlyGlyGlySerIleGlyProLeuVal
                                                                                                                                                                                                                                                                                                  148 --------GTCCAGCTAACAGGGGTCAAGAACTAATAATGATCCAGCAG
                                                                                                                                         GTGGGGCCGCAGGAGCAGCAGCTCAGCCTCTGGG---CCTGGGGCTTCC---CCTGGT
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Sequence 49, Application US/11053100

Sequence 49, Application US/11053100

Sequence 49, Application US/11053100

TUTLE OF UNEWATION: PUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

TITLE OF INVENTION: PUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

FILER REFERENCE: 4176-101 CIP

CURRENT APPLICATION NUMBER: US/11/053,100

CURRENT APPLICATION NUMBER: US 09/812,382

PRIOR FILING DATE: 2001-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

NUMBER OF SEQ ID NOS: 58

NUMBER OF SEQ ID NOS: 58
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Matches:
Conservative:
Mismatches:
Indels:
  Conservative:
Mismatches:
Indels:
                                                                                                    US-10-712-629B-2 (1-746) x US-11-053-100-48 (1-624)
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Best Local Similarity:
Query Match:
Percent Similarity:
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LENGTH: 774
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294 SeralaalaValalaThrThrLeuAsnGlyAsnSerValPheGlyGlyAlaGlyAlaAla 313
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353 oLysProAlaGlyValLeuProProLysLeuTyrGlnLeuThrProLysProPheAlaPr 373
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nHisMetLeuProGlyGlnAsnGlnPheLeuLeuProGlyAlaProAlaValGlnLeuPr 483
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256 GlnValProVal-----SerGlyTyrLeuAlaSerAlaAlaGlyProSerGluProVal
                                           274 ThrLeuAlaSerAlaGlyValSerProGlnGlyAlaGlyLeuValIleGlnLysAsnLeu
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CENDICACTION NO. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
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US-10-821-234-1182
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|329 ProGlyProSerGlyArgSerGlyProProGlyProLyBGlyGluArgGlyGluLyBGly 1348
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Mismatches:
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Matches:
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Gaps:
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1182
LENGTH: 1874
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US-11-053-100-50
; Sequence 50, Application US/11053100
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108.00
33.92%
29.52%
7.86%
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US-10-821-234-1182
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Best Local Similarity:
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DB:
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NAME/KEY: MISC_FEATURE
LOCATION: (1)._[(775)
OTHER INFORMATION: pET15b-SD6-ELP1-90-TEV-Estrogen receptor ligand binding domain
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APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Faul O.
TITLE OF INVENTION: Ztrfr14, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REFERENCE: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: US 09/812,382
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.3
SEQ ID NO 51
LENGTH: 775
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                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Construct
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GluileLeuMetile 569
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105.50
41.38%
26.21%
7.68%
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ORGANISM: Artificial
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Best Local Similarity:
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OTHER INFORMATION: pF715b-SD5-ELP1-180-throm-Estrogen receptor ligand binding domain
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US/11/053,100
CURRENT FILING DATE: 2005-02-08
PRIOR PILING DATE: 2006-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PARENTIN NUMBER: US 60/190,659
PRIOR FILING DATE: 2000-03-20
SOFTWARE: PARENTIN NUMBER: US 60/190,659
FRIOR PILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PARENTIN VETRION 3.3
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TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
TITLE REPERENCE: 4176-101 CIP
CURRENT APPLICATION NUMBER: US.11/053,100
CURRENT FILING DATE: 2005-02-08
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Matches:
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Mismatches:
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FEATURE:
OTHER INFORMATION: Synthetic Construct
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42.97%
25.00%
7.82%
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Best Local Similarity:
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Pred. No.:
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pGlyAsnLysGlyGluProGlyValValGlyAlaValGlyThrAlaGlyProSerGlyPr 638
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                                                                    GCTGGTCCTGCGGCCTCTTGATGCGCGTGTAGGACAGCAGCGCCTCCACGTAGGGCTGCT
                                                                                                                                681 GCAACGCCTCCACGCGCCCGGCTCCTGCACGTTGGGCCGGTCGGCCGAGAAGATGTTGA
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                                    US-10-712-629B-2 (1-746) x US-10-821-234-1431 (1-1366)
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US-10-821-234-1431
i Sequence 1431. Application US/10821234
i Publication No. US20050255114A1
i Publication No. US20050255114A1
i GENERAL INFORMATION:
i APPLICANT: Labar, Ivan
i APPLICANT: Andarmani, Susan
i APPLICANT: Tang, Y. Tom
i TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
i TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
i CURRENT FILING DATE: 2004
i CURRENT FILING DATE: 2003-04-07
i PRIOR FILING DATE: 2003-04-07
i NUMBER OF SEQ ID NOS: 1704
i SOFTWARE: pt_SEQ_genes Version 1.0
i SEQ ID NO 1431
LENGTH: 1366
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Indels:
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PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEC ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 308
TYPE: PRT
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US-10-967-527A-30
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CORGANISM: Mus musculus
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Sequence 5, Appl
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-424-599-210074
US-10-437-965-158893
US-10-425-114-42461
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28	279.5	7.5	384	4	US-10-425-115-219332	8	Sequence	219332,	
29	276.5	7.5	579	4	US-10-425-114-56872		Sequence	56872, A	
30	276.5		579	4	US-10-425-115-216734	4	Sequence	216734,	
31	274.5		189	ഹ	US-10-450-763-53352		Sequence	53352, A	
32	271.5		357	4	US-10-425-114-69939			69939, A	
33	266.5		668	4	US-10-425-115-210165	'n			
34	261.5		541	4	US-10-425-114-72403			72403, A	
35	255		893	4	US-10-425-115-288920	0		288920,	
36	252.5		913	4	US-10-437-963-125705	ıo		125705,	
37	241.5		997	4	US-10-437-963-181788	60		181788,	
38	232		349	4	US,-10-425-114-37462			37462, A	
39	232		380	4	US-10-425-114-71856				
40	227.5		225	4	US-10-425-115-266317	7		266317,	
41	208	5.6	1057	4	US-10-108-260A-3230			3230, Ap	
42	202.5	S	311	4	US-10-767-701-39873			39873. A	
43	201.5	5.4	217	4	US-10-424-599-172208	œ		172208,	
44	199	5.4	837	4	US-10-094-749-2698			2698, Ap	
45	196	5.3	184	4	US-10-767-701-32398				
					ALIGNMENTS				
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Length 693; Indels

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301 301 361

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181 TVMHQVWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIKE ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDR1HMAFAPVTPALPSDDR1T

61 AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC 120

61 AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFVTHWRC

1 VIQCQSCVQAAGEVGVLTGHSQKSRRSPLEEKQLEEEDSSATSEEGGGGGPGPEASLNKGL

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241 ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRIT 300

NILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPRPK 360

NILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPRPK

HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLDSTA

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61 AXHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC 120
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; Sequence 5, Application US/20030027300A1
; GENERAL INFORMATION:
; APPLICANT: THOOMPSON, Catherine C.
; TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
; FILE REFERENCE: Thompson-20263/0243435
; CURRENT APPLICATION NUMBER: US/10/024,368
; CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/201-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/287,354
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/090,888
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PATENTIN US: 2.0
; SOFTWARE: PATENTIN US: 2.0
; SOFTWARE: ACCOUNTY OF SEQ ID NOS: 10
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                                                            FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLASYLP
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HGPHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLDSTA
                                                                                                                        LGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLS
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                                                                                                                                                                                                                                                                                                                                 94.8%; Score 3510; DB 4.
ilarity 95.1%; Pred. No. 9e-265;
Conservative 11; Mismatches 23
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Matches 659; Conserv
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; ORGANISM: Rat
US-10-024-368-5
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10024368

publication No. US20030027000A1

GENERAL INFORMATION:

APPLICANT: THOMPSON, Catherine C.

TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN

TITLE REFERENCE: Thompson-20263/024345

CURRENT FILING DATE: 2001-12-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-07

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-07

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATCHTON VOWER: 2.0

SOFTWARE: PATCHTON VOWER: 2.0

SOFTWARE: PATCHTON VOWER: 2.0
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                                                                                                             GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAGLRR
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                                                  FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLASSLPLPEYCAHQGKLNLASYLP
                                                                                              LGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLS
                                  FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLASYLP
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Pred. No. 3.2e-278;
1; Mismatches 3;
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Best Local Similarity 99.4
Matches 689; Conservative
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US-10-024-368-6
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                                                                                CPRRGFHLFQEHWRQGQPVLVSGIQRTLQGNLWGTEALGALGGQVQALSPLGPPQPSSLG
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 TNILDSIIAOVVERKIOEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLOEPR-
                    794 TNILDSIIAQVVERKIQEKALGPGERAGPGLRKGLGLPLSPVRPRLPPPGALLWLQEPQP
                                                                - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
                                                                                                                              STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
                                                                                                                                               914 SITFWEGFSWPELRPKSDEGSVLLLHRALGDEDTSRVENLAASLPLPEYCALHGKLNLAS
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83.4%; Score 3089.5; DB 4;
Best Local Similarity 83.0%; Pred. No. 6.3e-232;
Matches 578; Conservative 40; Mismatches 75;
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Publication No. US20030077614A1
GENERAL INFORMATION:
APPLICATY: Christiano, Angela
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 0575/62637A
CURRENT FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-122-013-17
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                            361 HGFHLFQEHWRQGQPVLVSGIQKTLRLSLMGMEALGTLGGQVQSLTALGPPQFTNLDSTA
                                                                                                               GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDSGLRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10024368
; Publication No. US2033027300A1
; Grenkal INFORMATION:
    Grenkal INFORMATION:
    TITLE OF INVENTION: UMAN HUMAN HAIRLESS GENE AND PROTEIN
    FILE REFERENCE: Thompson-20263/024345
; CURRENT PAPLICATION NUMBER: US/10/024,368
; CURRENT FILING DATE: 2004-12-21
    PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/287,354
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-07
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: PATENTIN VER. 2.0
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TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
FILE REFERENCE: Thompson-20263/024343.5
CURRENT APPLICATION NUMBER: US/10/024,368
CURRENT FILING DATE: 2001-12-21
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: US/09/287,354
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-07
RIOR FILING DATE: EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALCHING DATE: LANGE APPLICATION NUMBER: US 60/080,888
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-07
SOFTWARE: PALCHING DATE: 2.0
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82.9%; Pred. No. 5.4e-231;
iive 37; Mismatches 79;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                            QIKEBREQDNSESPNGRISPLVSQNNEQGSTLRDLLITITAGKLRVGSTDAGIAFAPVYSM
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                                                                        ----AEDGAGR-SPLPC----PSLCELLASTAVKLCLGHDRIHMAFAPV---
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Sequence 20, Application US/10193874

Publication No. US20030064396A1

GENERAL INFORMATION:

APPLICANT: Jenapharm GmbH & Co. KG

TITLE OF INVENITION: Comodulators of Nuclear Receptors

FILE REFERENCE: 52145

CURRENT FILING DATE: 1998-11-18

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 728.5; DB 4; 29.1%; Pred. No. 4e-47;
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19.7%; Score 728.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 4e-47;
Matches 219; Conservative 118; Mismatches 267;
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                                                                                                                                        -TPALPSDDRITNILDSIIAQVVERKI-----
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                                                                      STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPBYCAHQGKLNLAS 477
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914 STTFWEGFSWPELRPKSDEGSVLLLHRAFGDEDTSRVENLAASLPLPEYCALHGKLNLAS
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                                                                                                                    359 - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
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19.7%; Score 729; DB 4; Length 1265,
Best Local Similarity 29.2%; Pred. No. 1.9e-47;
Matches 219; Conservative 117; Mismatches 270; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 795, Application US/10408765A
| Publication No. US20040101874A1
| General Information |
| General Information |
| APPLICANT: Fahy, Eoin D. |
| APPLICANT: Fahy, Eoin D. |
| APPLICANT: Gleon, Bradford W. |
| APPLICANT: Gleon, Bradford W. |
| APPLICANT: Gleon, Bradford W. |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Warnock, Dale E. |
| TILE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION |
| TILLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION |
| TILLE OF INVENTION: TOBOTIFIED IN THE MITOCHONDRIAL PROTEOME |
| CURRENT APPLICANTION NUMBER: US/10/408,765A |
| NUMBER OF SEQ ID NOS: 2003-04-04 |
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                 1698 LDAMHTLREKYGIKSHCHCTNKQNLQVGNFPTWNGVSQVLQNVLNHSNKISLCMPESQQQ
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19.7%; Score 728.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 4.8e-47;
Matches 219; Conservative 118; Mismatches 267;
 180 STVMHQAWAKFDIRGHCFC----QVDARVWAPGDGGQQ-
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                                                                                                                                                    290 -TPALPSDDRITNILDSIIAQVVERKI-----
                                                   219 KTPPTPQPSCNGDSNRTKDIKEE---TPDSTESP
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CORGANISM: Homo sapiens
US-10-193-874-14
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   1432 LDAMHTLREKYGIKSHCHCTNKQNLQVGNFPTMNGVSQVLQNVLNHSNKISLCMPESQQQ 1491
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19.7%; Score 728.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 4.7e-47;
Matches 219; Conservative 118; Mismatches 267;
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                              KTPPTPQPSCNGDSNRTKDIKEE---TPDSTESP-
                                                                                                                                 -TPALPSDDRITNILDSIIAQVVERKI-----
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TITLE OF INVENTION: Comodulators of Nuclear
FILE REFERENCE: 52145
CURRENT APPLICATION NUMBER: US/10/193,874
CURRENT FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 17
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US-10-193-874-17
is Sequence 17, Application US/10193874
is Publication No. US20030064396A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-193-874-17
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1861 OKCGFVVCLDCYK----AKERKSSRDKELYAWMKCVKGOPHDHKHLMPTQIIPGSVLTDL 1916
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US-10-193-814-15

§ Sequence 15, Application US/10193874

§ Publication No. US20030064396A1

§ GENERAL INFORMATION:

APPLICANT: Jenapharm GmbH & Co. KG

† TITLE OF INVENTION: Comodulators of Nuclear Receptors

FILE REFERENCE: 52145

CURRENT APPLICATION NUMBER: US/10/193,874

; CURRENT FILING DATE: 1998-11-18

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIN Ver. 2.1

; SEQ ID NO 15
                                                                                                                 180 STVMHQAWAKFDIRGHCFC----QVDARVWAPGDGGQQ-----
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CURRENT FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 2540
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19.7%; Score 728.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 5.4e-47;
Matches 219; Conservative 118; Mismatches 267;
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                                                     STVMHQAWAKFDIRGHCFC----QVDARVWAPGDGGQQ-
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Sequence 16, Application US/10193874
Publication No. US20030064396A1
GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALTHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASISEO for Windows Version 4.0
SEQ ID NO 588
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                                                    1630 LDAMHTLREKYGIKSHCHCTUKQNLQVGNFPTMNGVSQSQQQNTPPKSEK--NGGSSPES
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19.3%; Score 714; DB 5; Length 2353;
Best Local Similarity 29.1%; Pred. No. 6.6e-46;
Matches 219; Conservative 117; Mismatches 263; Indels 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 MEALG-TLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKD 450
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                                                                                                                                                                                                                                                                                                                                                                       -----AEDGAGR-SPLPC----PSLCELLASTAVKLCLGHDRIHMAFAPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 NSHRGH-LGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLSGLDGEGLWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PGSQTSTVWHVFRAQDAQRIRRFLQMVC-PAGAGTL---EPGAPGSCYLDAGLRRR
                                                      SHCSHRLCVACGRIAGAGKNREKTGSQEQHT-DDCAQEAGHAACSLILTQFVSSQALAEL
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19.4%; Score 719; DB 5; Length 2210;
Best Local Similarity 30.0%; Pred. No. 2.4e-46;
Matches 207; Conservative 108; Mismatches 250; Indels 124;
                                                                                                                                                            STVMHQAWAKFDIRGHCFC----QVDARVWAPGDGGQQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2511 LLKEEINYDDKL---QVKNILYHAVKEMVRALK 2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 589, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
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US-10-719-993-589
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SNGTH: 2210
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27;

Gapa

Search completed: November 25, 2005, 22:17:09 Job time : 171 secs



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November 25, 2005, 22:03:15; Search time 44 Seconds (without alignments) 1515.414 Million cell updates/sec
                                                                                                                                                                                               US-10-712-629B-18
3704
1 VTQCQSCVQAAGEVGVLTGH......MDRAVFQAVKAAVGALQEAK 693
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              283416 seqs, 96216763 residues
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                   Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	r.	hairless protein		ical pro			hypothetical prote	DNA-binding protei	early nodulin bind	ENBP1 protein - ba	hypothetical prote		Ĕ	c	Ω	Ω		Bassoon protein -	tastin - human	VGF8a protein prec	hypothetical prote		pqqF protein - Kle	ч	fatty-acid synthas	diacyldlycerol kin	primosomal protein	gene APXL protein	Bassoon protein -	
SUMMARIES		148378	\$28499	D86254	T01440	B85013	T10539	T06461	T10955	T43213	T05151	F86222	A54277	S39162	S39161	T42710	833561	T42761	138487	805381	T46289	A24938	S20458	JC4978	G01880	S71467	A83015	137183	T42730	
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	engt	1182	1214	851	906	730	730	1629	1641	1701	728	950	2414	2440	2441	1479	594	3938	778	711	862	907	761	442	2509	728	739	1616	3942	0
di	ery	99.4	v	9.1	9.1	9.9	9.9	6.5	•	•	5.5	4.9			3.9	•	•	•	3.3	•	•	•	3.1	•	•		3.0			
	Sco	3682	604.5	338	337	246	246	240.5	237	232	205.5	181.5	146.5	145.5	145.5	127.5	122.5	122	121	119	117.5	116	115	114	113.5	112.5	112.5	112.5	111.5	
		1	7	3	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

repair protein XPG	hypothetical prote	microtubule-associ	giant protein p619	janusin precursor,	hypothetical prote	UL37 protein - hum	complement compone	probable non-ribos	mating type A alph	still life protein	coagulation factor	hypothetical prote	Carbon catabolite	clathrin assembly	CDEP protein - hum
A57650	T37128	A37127	S71752	A45445	T00271	WMBEH7	150806	F83345	B46203	T13704	T42763	B72468	JN0785	S36326	JC5795
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1170	57,	107	486	13	111	11	167	21	80	207	213	3.	4	8	10
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3.0	110.5 3.0 573	3.0	3.0		2.9	2.9	2.9	2.9	2.9	2.9	2.9	5.9	2.9		2.9

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RESULT 1

148378	4
hairless	ss protein - mouse
C;Species:	les: Mus musculus (house mouse) . 02-Jul-1996 #semmence revision 02-Jul-1996 #text chance 09-Jul-2004
C; Acces	ל #פכלתכווכב ופיובוטון טב-טעו- בזיזט הכהגר בוומווטפ 3
R, Cache	R;Cachon-Gonzalez, M.B.; Fenner, S.; Coffin, J.M.; Moran, C.; Best, S.; Stoye, J.P.
Proc. r A:Title	FIGO. Natl. Acad. Sci. 0.5.4. 9!, //1/-//ll, 1994 A:Title: Structure and expression of the hairless gene of mice.
A; Refer	number: 148378; MUID:94329587; PMID:8052649
A;Status: pre	ssion: 1483/8 18: preliminary; translated from GB/EMBL/DDBJ
A, Molecule	A; Molecule type: mRNA
A; Crose	A;Cross-references: UNIPROT:Q61645; UNIPARC:UPI000028C24; EMBL:Z32675; NID:g531706; PI
Query	Query Match 99.4%; Score 3682; DB 2; Length 1182; Best Local Similarity 99.4%; Pred. No. 3.38-257;
Matches	89; Conservative 1; Mismato
δŏ	1 VTQCQSCVQAAGEVGVLTGHSQKSRRSPLEEKQLEEEDSSATSEEGGGGGPGPFASLNKGL 60
ΩÞ	490 VTQCQSCVQAAGEVGVLTGHSPLEEKQLEEEDSSATSEEGGGGGGGPGFEASLNKGL 549
ò	61 AKHLLSGLGDRLCRLLRKEREALAWAQREGGGPAMTEDSPGIPHCCSRCHHGLFNTHWRC 120
QQ	SSO AKHLLSGLGDRLCRLLRKERRALAWAQREGGGPAMTEDSPGIPHCCSRCHHGLFNTHWRC 609
δ	121 SHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAELS 180
qq	610 SHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAELS 669
ò	181 TVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIKE 240
qa	610 TVMHQVWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIKE 729
ď	241 ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRIT 300
qu	730 ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRIT 789
ò	301 NILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLMLQEPRPK 360
οp	790 NILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSFVRTRLSPPGALLMLQEPRPK 849
ò	361 HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGFPQPTNLDSTA 420
qq	850 HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQTLTALGFPQPTNLDSTA 909
č	421 FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLASYLP 480
Ор	910 FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLASSLPLPEYCAHQGKLNLASYLP 969

```
Pypothetical protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: B6254
C; Accession: B6254
C; A: Theologis, A: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Marter, J.L.; Hudses, B.; Hutzar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Yr; Lin, Xr; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Yr; Lin, Xr; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A; Atthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Refrence number: A6141; MUID:21016719; PMID:11130712
A; Accession: 16:254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-851 <STO>
A;Cross-references: UNIPROT:065384; UNIPARC:UPI0000A00D6; GB:AE005172; NID:g3157933; P
C;Genetics:
                                    1073 BFLKKVSEEQGQENPADH---DPIHDQSWYLDRSLRKRLYQEYGVQGWAIVQFLGDVVFI 1129
                                                                                                                                                                                                             |||||||| | | | | | | : |:|||
1130 PAGAPHQVHNLYSCIKVAEDEVSPEHVKHCFWLTQEFRHLSQTHTNHEDKLQVKNVIYHA 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 LS----LWGMEAL-----GTLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETR----P 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKEPT----EKTPPTPQPSCNGDSNRTKDIKEETPDSTESPAEDGAGRSPLPCPSLCEL 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 KLDEGSVLLLHRTLGDKD---ASRVQNL-----VSSLPLPEYC-AHQGKLNLASYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 SGLRKGLSLPLSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLV-SGIQKTLR
                                                                                                                                                                                    PAGAPHOVOGLVSTISVTOHFLSPETSALSAQLCHQGASLPPDH--RMLYAQMDRAVFOA
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             -- EGLWSPGSQTSTVWHVFRAQDAQRIR
                                                                                                    571 RFLQMVC-----PAGAGTLEPGAPGSCYLDAGLRRRLREFWGVSCWTLLQAPGEAVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
9.1%; Score 338; DB 2; Length 851;
Best Local Similarity 22.2%; Pred. No. 2.5e-16;
Matches 148; Conservative 91; Mismatches 192; Indels 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHAEAQLPPWYRAQKDFLSGLDG-
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Ridogoription: Analysis of a murine germ cell-specific transcript that encodes a putativ A; Reference number: $28499
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A; Respecimental source: strain Sprague Dawley
C; Keywords: DNA binding; zinc finger
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LGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLS
                                                                                    GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAGLRR
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.larity 26.7%; Pred. No. 2.5e-35;
Conservative 114; Mismatches 289;
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hypothetical protein AT4g00990 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (CiSpecies: Arabidopsis thaliana (mouse-ear cress) (CiSpecies: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004 (CiAccession: B85013 ** Arabidopsis Genome Sequencing Consortium, The Cold Sprinature 402, 769-777, 1999 ** Arabidopsis Genome 4 of the plant Arabidopsis thaliana. Aireference number: A85001; MUID:20083488; PMID:10617198 ** Arabidopsis thaliana. Aireference number: A85001; MUID:20083488; PMID:10617198 ** Arabidopsis thaliana. Airesidua: preliminary Airesidua: preliminary Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thaliana. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thalianae. Airesiduae: 1-730 ** Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                               S---QEQISSVKALKQKHKLQNKVDKQSTEDCNEKEEEEEEELNMPEISSNENEFTGSAL 751
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                                                                                                             472 KLNLASYLPLGLTLHPLEPQLWAAYGVNSH--RGHLGTKNLCVEVSDLISILVH-AEAQL
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19.3%; Pred. No. 9e-10;
tive 91; Mismatches 236; Indels 318;
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Matches 154; Conservative
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C.Accession: T01440
R.Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Concologis, A.; Ecker, J. R.
submitted to the EMBL Data Library, January 1998
A.Description: Genomic sequence for Arabidopsis thaliana BAC F2401.
A.Refearence number: Z14211
A.Accession: T01440
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
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                                                                                                                                             657
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                                                                                                         QLPPWYRAQKD----FLSGLDGEGLWSP----GSQTSTVWHVFRAQDAQRIRRFLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPHQVQGLVSTISVTQHFLSPETSALSAQLCHQGASLPPDHRMLYAQMDR------
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                                                                                                                                                                                                                                                                                                                                           ----MVCPAGAGTLEPGAPGSCYLDAGLRRRIREEWG----VSCWTLLQAPGEAVLVPA
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                                                                      LGLTLHPLEPQLWAAYGVNSH--RGHLGTKNLCVEVSDLISILVH-
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A;Map position: 1
A;Introns: 239/2; 272/3; 317/1; 338/2; 682/3; 832/1; 860/3
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A;Residues: 1-1629 %AT>
A;Cross-references: UNIPROT:004698; UNIPARC:UPI000009FC7F; EMBL:X98744; NID:e995233; PI:
A;Cross-references: UNIPROT:004698; UNIPARC:UPI000009FC7F; EMBL:X98744; NID:e995233; PI:
A;Experimental source: cv. Alaska
C;Genetics:
C;Genetics:
A;Genome: nuclear
C;Keywords: chloroplast
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                                                                                                        : |:|| :|| ::| |:|| 301 INLHQFEGYLEGRMHKNGWPEMLKLKDWPPSDLFEKRLPRHNA----BFIAALPFFDYT 356
                                                                                                                                                                               | | : ::||
416 AKVEIPPVKYQNIKVHQKKYABAMLQKQQYSGQVKBASELENKSMKEVDESKKDLKDKAA 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding protein PD3, chloroplast - garden pea C; Species: Pisum sativum (garden pea) C; Species: Pisum sativum (garden pea) C; Date: 23-Apr-1999 #text_change 09-Jul-2004 C; Accession: T06461 Existo, N. submitted to the EMBL Data Library, June 1996 A; Reference number: 215695 A; Accession: T06461 A; A; Accession: T06461 A; A; Accession: Preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                    617 PGEAVLVPAGAPHOVOGLVSTISVTQHFLSPETSALSAQLCHQGASLPPDHRMLYAQMDR
           ---GMEALGTLGGQVQSLTALGPPOPTN
                                                                                                                                                        468 -AHOGKINIASYLPLGLTLHPLEPQLWAAYGVNS--HRGHLGTKNLCVEVSDLISILVH-
                                                                                                                                                                                                                                                                                                                                                                               -----TVWHVFRAQDAQRIRRF
                                                                                 ---SHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYC
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                                                                                                                                                                                                                                  ----WYRAOKDFLSGLDGEGL----
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701 LELKKIALYAASSAIREVK 719
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: T10539
R; Bevan. M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Be submitted to the Protein Sequence Database, June 1999
A; Reference number: Z17080
A; Accession: T10539
A; Accession: T10539
A; Accession: T10539
A; Accession: T10539
A; Mose-references: UNIPARC: UNIPARC: UPI00000ABSES; EMBL: AL080237; GSPDB: GN00062; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 QGPAMTEDSPGIPHC-----CSRCHHGLFNTHWRC--SHCSHRLCVACGRIAGAGK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NREKTGSQ--EQHTDDCAQEAGHAACSLILTQFVSSQALAELSTVMHQAWAKFDIRGHCF 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                  648 LGEAVFIPAGCPHQVRNR----QVALDFVAPESVEECLRLTQEFRRLPKDHS---SSEDK 700
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                                                                                                                                 301 INLHQFFEGYLEGRMHKNGWPEMLKLKDWPPSDLFEKRLPRHNA----EFIAALPFFDYT
                                                                                                                                                                                                                      476 NEEQSNNSSRPSGSGEAEKVIISKGIARIRELSHSYVYKHMLLNMENGLMMPTLLATPPC
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                                                                                                                                                                                                                                                                                                                               -AHOGKINLASYLPLGLTLHPLEPQLWAAYGVNS--HRGHLGTKNLCVEVSDLISILVH-
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                                                                                                          ---WYRAQKDFLSGLDGEGL---
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A;Note: intron positions not resolved
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                                                                                                          524 AEAQLPP----
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Db 994		QY 544	Db 1534 ILVINEKHKKQLKIEYĞVEPWIFECHLGBANFIPAĞCPHQYRNRKSCİKVAMDFVSPENV 1593 Qy 651 ALSAQLCHGGASLPPDRRMIYAQMDRAVFQAVK 683	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Rolecule type: DNA A;Rosidues: 1-1701 cGHR> A;Cross-references: UNIPROT:082022; UNIPARC:UPI00000A1840; EMBL:AJ002479; NID:e1317985; A;Experimental source: cultivar Jemalong C;Genetics: A;Cene: ENBPl A;Introns: 856/3; 900/2; 933/3; 978/1; 1000/2; 1220/3; 1329/3; 1585/3; 1610/1; 1638/3;
QY 279 HDRIHMAFAPUTPALPSDDRITNILDSIIAQUVERKIQEKALGPGLRAGSGLRKGLSLPL 338 Db 1033 VEELTVKYQPPIADLSLGGSECRSFEEDVAGNSARKAASRETG	Qy 478 YLPLGLTLHP-LEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVH-AEAQLPPWY- 532 Db 1223 KLPAULKPDLGPKTYIAYGTSDELSRGDSVTKLHC-DISDAVNLTHTAEVKPPPWS 1279 Qy 533RAQKDP	555	RESULT 8 T10955 early nodulin binding protein 1 - spring vetch C; Species: Vicia sativa (spring vetch, tare) C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C; Accession: T10955 R; Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgard, N.; Larsen, K.; Yang, W.C.; Biss submitted to the EMBL Data Library, December 1995 R; Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgard, N.; Larsen, K.; Yang, W.C.; Biss submitted to the EMBL Data Library, December 1995 R; Christiansen, A.; Farstone Trovel trype of DNA binding protein interacts with a conserved sequence in A; Reference number: Z1728 A; Reference number: Z1728 A; Residues: L-1641 cCHR> A; Residues: L-1641 cCHR> A; Residues: L-1641 cCHR> A; Residues: L-1641 cCHR> A; Residues: L-1641 cCHR> A; Residues: L-1641 cCHR> A; Ross-references: UNIPROT: Q41700; UNIPARC: UPI00000A5C40; EMBL: X95995; NID: g1360633; PIC; Reywords: DNA binding	Query Match Best Local Similarity 18.3%; Pred. No. 1.1e-08; Bast Local Similarity 18.3%; Pred. No. 1.1e-08; Matches 151; Conservative 66; Mismatches 229; Indels 378; Gaps 24; Qy 106 CSRCHGLFNTHWRCSHSPRLCVACGRIACAGGNRERTGSGEQHTDDCAGEAGH 160

25;

Gaps

211;

Length 728 Indels ----PCPSLCE

SPPSP-----TTSNVSSPCDVKVGEEPISMIKRRFRSKNIEPLP-IGK 206

369

--CTRSSSVLRLNSDQDQSQESLSRKVGSVKCSNGIKSPKVLLDFHQNNLEH----FQTH 312

WRQGQPVLVSGIQKTLRLSLWGMEA----

TLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQN 456 LVSSLPLPEYC-AHQGKLNLASYLPLGLTLHPLEPQLWAAYGVNSHRGHL----GTKNL

----- AEAQLPPWYRAQK----D 537

| | :: | | :: | | GFETCDMVDILLYVTETPVSTNQICRIRKLMKNIGRVRSKNPAKGRESRFDKGKKRDRLD

CVEVSDLISILVH------

FLSGLDGE-----GLWSPGSQ------

524

-----TSTVWHVFRAQDAQRIR 570

584

RF-----LQMVCPAGAGTLEPGAPGSCYLDAGLRRRLREEWGVSCWTLLQAPGEAVLV 623

PAGAPHOVOGLVSTISVTQHFLSPETSALSAQLCHQGASLPPDHRMLYAQMDRAVFQAVK 683

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267 LLASTAVKLCLGHDRI-HMAFA----PVTPALPSDDRITNILDSIIAQVVERKIQEKAL 320
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A;Reference number: Z15400
A;Accession: T05151
A;Molecule type: DNA
A;Residues: 1-728 «BEV»
A;Cross-references: UNIPROT:O65408; UNIPARC:UPTO0000A1A08; EMBL:ALO22603
A;Residues: 1-728 «BEN»
A;Accession: T05185
A;Molecule type: DNA
A;Residues: 1-728 «BEN»
A;Cross-references: UNIPARC:UPI00000A1A08; EMBL:AL031187
A;Experimental source: cultivar Columbia; BAC clone T6K22
C;Genetics:
C;Genetics:
A;Molecule type: DNA
A;Introns: 208/3; 253/1; 298/1; 361/3; 471/3; 603/3; 628/1; 656/3; 696/3
A;Note: F18E5.50; T6K22.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 DYSSSDSESSQHCLGAKCRGSEFEGEERESCNYSCEEESLSNTYGAQWDVFQKQDVSKLL
                                                                                                                                                                                                                                                                                                                                                                                                                     207 MQDSQSVRSDI--DRVLHLHYAVCMLLPVLKEINAEHKVE-----VENDAEKKVDLQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 GPGLRAGSGLR-----KGLSLPLSPVR--TRLSPPGALLWLQEPRPKHGFHLFQEH
                                                                                                                                                                                                                                                                                                                                      220 TPPTPQPSCNGDSNRTKDIKEETPDSTESPAEDGAGRSPL----
                                                                                                                                                                                                                                                                         Query Match 5.5%; Score 205.5; DB 2; Best Local Similarity 19.8%; Pred. No. 7.4e-07; Matches 121; Conservative 88; Mismatches 190;
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                                                                                                                                                     ---ETIAWRAETNGSIPCPPKARGCGTATL---SLRRLFKANWIEKLTRDAEELTIKYQ 1108
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                                                                                                                                   LFNTHWRC--SHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQF 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTLGDKDASRVQNLVSSLPLPEYC-AHQGKLNLASYLPLGLTLHP-LEPQLWAAYGV--N 499
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                                                                       -----CSRCHHG
                                                                                                                                                                                                                                                            231 DSNRTKDIKEETPDSTESP--AEDGAGRSPLPCPSLCELL-ASTAVKLCLGHDRIHMAFA
                                                                                                                                                                                                                                                                                                                           PVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSP
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                                          Gaps
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                                        370;
        Length 1701;
        Query Match 6.3%; Score 232; DB 2; Length 177
Best Local Similarity 19.6%; Pred. No. 2.7e-08;
Matches 171; Conservative 71; Mismatches 259; Indels
                                                                       71 RLCRLLRKEREALAWAQREGQ------GPAMTEDSPGIPHC---
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hypochetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Apate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: F66222 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
RESULT 11
                                         hypothetical protein F18E5.50 - Arabidopsis thaliana
N;Alternate names: hypothetical protein T6K22.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05151; T05185
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
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669

AAVGALQEAK 693 SKANKIEVKK

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Rickner, R.; Ewen, M.E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, J.B.; Livi Genes Dev. 8, 869-884, 1994
A.Title: Molecular cloning and functional analysis of the adenovirus ElA-associated 300 A.Reference number: A54277
A.Accession: A54277
A.Accession: A54277
A.Accession: A54277
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-2414 < ECKs
A.Residues: 1-2414 < ECKs
A.Residues: Lost a ECKs
A.Residues: Lost a Ender a Elambation 941-Ser is shown after 961 and consequently, residu Rilumblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.
Nature J.Y. 86-88, 1995
A.Title: Adenoviral ElA-associated protein p300 as a functional homologue of the transc
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A, Status: preliminary
A, Molecule type: protein
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iive 70; Mismatches 242;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-950 <STO>
A; Cross-references: UNIPROT:004024; UNIPARC:UPI00000A8940; GB:AE005172; NID:g2342679; PI
C; Genetics:
A; Map position: 1
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C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A54277; S60344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.9%; Score 181.5; DB 2;
Best Local Similarity 21.1%; Pred. No. 5.6e-05;
Matches 128; Conservative 76; Mismatches 208;
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DB 2; Length 2414;

-----PQPÓQĽQŚG 2009

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A;Accession: S39161
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-2441 <CHR>
A;Residues: 1-2441 <CHR>
A;Cross-references: UNIPARC:UPI0000029625; GB:S66185; NID:G435854; PIDN
C;Superfamily: transcription coactivator (REB-binding protein; bromodomain homology
P;1112-1169/Domain: bromodomain homology <BRO>
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                                                                                                                                                                                                                                                                       2106 AKYVANQPGMQPQPGLQSQPGMQPQPGMQOPSLQNLNAMQAGVPRPGVPPPQPAMGGLN 2165
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1619 QKLYATMEKHKEVF-FVIHLHAGPVISTQPPIVDPDPLLSCDLMDGRDAFLTLARDKHWE 1677
                                                                                                                                             1678 FSSLRRSKWSTLCMLVELHTQGQDRFVYTCNECKHV-ETRWHCTVCEDYDLCINCYNTK 1736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEGLW----SPGSQTSTVWHVFRAQDAQRIRRFL-----QMVCPAG----AGTLEPG 587
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Cispecies; Wus musculus (house mouse)
Cispecies: Frb. 1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Ciaccession: S39161
R;Chrivia, J.C.; Kwok, R.P.S.; Lamb, N.; Hagiwara, M.; Montminy, M.R.; Goodn
Nature 365, 855-869, 1993
A;Title: Phosphorylated CREB binds specifically to the nuclear protein CBP.
A;Reference number: S39161; MUID:94019866; PMID:8413673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------QVDARVWA---PGDGGQQK--EPTEKTP--PTPQPSCNGDSNRTKDI
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                                                                                                                                                                                                                                                                                                                                                                           170 FVSSQALAELSTVMHQAWAKFDIRG-
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A; Map position: 16p13.3-16p13.3
A; Map position: 16p13.3-16p13.3
A; Map position: 16p13.3-16p13.3
A; Mote: defects in this gene may result in Rubinstein-Taybi syndrome
C; Superfamily: transcription coactivator (REB-binding protein; bromodomain homology
C; Keywords: phosphoprotein; transcription; zinc finger
F; 462-661/Domain: Dromodomain homology eRRO-
F; 1111-1168/Domain: bromodomain homology eRRO-
F; 1111-1168/Domain: bromodomain homology eRRO-
F; 11707-1732/Region: zinc finger CCC motif
F; 1707-1732/Region: zinc finger CCC motif
F; 1707-1732/Region: zinc finger CCC motif
F; 1717-1732/Region: zinc finger CCC motif
F; 1771/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: mRNA
A, Residues: 1-2440 - CHR>
A, Residues: 1-2440 - CHR>
A, Residues: 1-2440 - CHR>
A, Residues: 1-2440 - CHR>
A, Access-references with the mouse sequence are shown
B, Lundblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.
R, Lundblad, J.R.; Kwok, R.P.S.; Laurance, M.E.; Harter, M.L.; Goodman, R.H.
A, Reference number: S60344; MUD: 95174889; PMID: 7870179
A, Reference number: S60345
A, Molecule type: protein
A, Residues: S74-670, T., 672-681 - CLUN
A, Molecule type: Drotein
A, Residues: S754-670, T., 672-681 - CLUN
A, Residues: S754-670, T., 672-681 - CLUN
A, Residues: S754-670, T., Bauwerse, H.G.; Saris, J.J.; Hennekam, R.C.; Masuno, M.; Tomm
Maure 376, 346-331, 1995
A, Title: Rubinstein-Taybi syndrome caused by mutations in the transcriptional co-activat
A, Reference number: 158096; MUID: 95356817; PMID: 7630403
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A.Residues: 352-356 <PET>
A.Cross-references: UNIPARC:UPI00001782EE, GB:U89354; NID:g1888537; GB:S78936; NID:g1041
A.Note: this translation is not annotated in GenBank entry S78936, release 112.0
A.Note: this sequence with a termination mutation is from a patient with Rubinstein-Tayh
A.Gene: GDB:CREBBP; RTS; CBP; RSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence revision 17-Nov-1995 #text_change 02-Aug-2002
C;Accession: S39162; S60345; Ī58096
R;Chrivia, J.C.; Kwok, R.P.S.; Lamb, N.; Hagiwara, M.; Montminy, M.R.; Goodman, Mature 365, 855-859; 1993
A;Title: Phosphorylated CREB binds specifically to the nuclear protein CBP. A;Reference number: S39161; MUID:94019866; PMID:8413673
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           LPLP---EYCAHQGKLNLASYLPLG-LTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSD
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N/Alternate names: CBP; RSTS; Rubinstein-Taybi syndrome (RTS) protein
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Pred. No. 0.073;
1; Mismatches 290;
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                                                                                                                                                                                                                                                                                                          568 RIRRFLQMVCPAGAGTLEPGAP 589
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Chem. 271, 21323-21330, 1996

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Artitle: Characterization of a novel member of the macrophage mannose receptor type C A; Reference number: 22235; MUID:96355501; PMID:8702911
A; Accession: 142710
A; Ascatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1479 < WUK>
A; Residues: 1-1479 < WUK>
C; Superfeamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II C; Keywords: membrane protein; receptor
F; 186-227/Domain: fibronectin type II repeat homology < 2FR>
                                                                                                                                                                                       1678
                                           42;
                                                                                               FSSLRRSKWSTLCMLVELHTQGQDRFVYTCNECKHV-ETRWHCTVCEDYDLCINCYNTK 1737
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                                                                                                                                                                                                                                                                                                                                                                                                          - PSCOKMKRV - - VQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHN 1850
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N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
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                                         Gaps
                                         301;
     Length 2441;
                                         Indels
3.9%; Score 145.5; DB 2;
18.6%; Pred. No. 0.073;
tive 101; Mismatches 290;
                                                                                                                                                  DRLCRLLRKEREALAWAQREGOGPAMTEDSPGIP---
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                                    Conservative 101;
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                                                                                                                                                                                                                                                                                                     396 QAEKRSWÓESKR-AČLRGGGDLLSIHSMAEL---EFITKÓIKQEVEELWIGLNDLKLOMN 451
                                                                                                                                                                                                                                                                                                                                                                                                                                      RLSQGAABEBHDCRKGWTWHSPSCYWLGED-----QVIYSDARRLCTDHGSQLVTIT 559
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                                                                                      SCEQQGADLLSITEIHEQTYINGLLTGYSSTLWIGLNDLDTSGGWQWSDNSPLKYLNWES
                                                                 SCVQAAGEV-----QKSRRSPLEEKQLEE
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ALIGNMENTS

RESULT 1

KIAA0930 protein; monocytes antigen CD14; sphingolipid activator protein; beta-symuclein; C11 protein; vesicle-associated membrane protein 2; aldolase A; CG1-106 protein; hypothalamus protein HSMVP1; alpha enolase; POM-2P3; quinone oxidoreductase; pumilio 1; VPS41; KIAA0614 protein; splicing factor CC1.4; ubiquitin; beta-mannosidase; hair growth. mouse; hairless protein; Hrt; ubiquitous receptor UR; MAP1A; Hairless protein interaction partner #35 DR; Toerner Ş ADO57501 standard; protein; 693 02-JUN-2003; 2003US-00452858 03-JUN-2002; 2002US-0385414P (PROC) PROCTER & GAMBLE CO (first entry) Gerwe GS, US2004086945-A1 Sreekrishna K, Mus musculus. 06-MAY-2004. 29-JUL-2004 ADO57501; AD057501

WPI; 2004-430095/40. N-PSDB; ADOS7500 New composition comprising mouse truncated hairless protein-human interacting partner protein or nucleic acid complexes, useful for screening test compounds that inhibit or enhance hair growth.

Example 1; SEQ ID NO 93; 60pp; English

The invention relates to a composition comprising a mouse truncated balitiess (HTL) protein-human interacting partner protein or nuclaic acid complex. The human interacting partner protein comprises a molecule selected from ubiquitous receptor UR, MAPIA, KIAA0930 protein, monocytes antigen CD14, aphingolipid activator protein, beta-synuclein, C11 protein, vesicle-associated membrane protein 2, aldolase A, CGI-106 protein, hypothalamus protein HSMNP1, alpha enolase, POM-2P3, quinone

ABU70953 ADD18797

of gene

Novel expression construct, useful in the diagnosis and treatment dermatological conditions, such as hair loss, contains a Hairless

Example, Fig 1, 48pp, English.

seguence.

(CARN-) CARNEGIE INST WASHINGTON

WPI; 2002-204622/26.

99US-00287354 98US-0080888P

07-APR-1999; 07-APR-1998;

gene

hair loss;

Mus musculus US6348348-B1

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oxidoreductase, pumilio 1, VPS41, KIAA0614 protein, splicing factor CC1.4, ubiquitin, beta-mannosidase. Also described are: methods of assaying a test compound for agonist or antegonist activity for the above composition; and methods of inhibiting or increasing hair growth on a surface in a subject. The present sequence represents a hairless protein interacting partner used in the composition.
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                                                                                                                                                                                                                                                                 acid molecules (HR) encoding such polypeptides. The invention also relates to the Hairless expression constructs which may be used in transcription assays. Sequences of the invention are used in diagnosis and treatment of dermatological conditions such as hair loss. They are also used in gene therapy. Polynucleotides of the invention can be used as probes for the detection of hair loss. The present sequence is mouse Hairless protein (Hr)
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Mouse; Hairless protein; Hr protein; HR gene; dermatological condition;

Mouse Hairless protein (Hr) (first

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Rattus norvegicus
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                                                                                                    1089
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970 LGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLS 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hairless, Hr; thyroid hormone receptor; hair growth; hair loss; pedigree; radiation hybrid; somatic cell hybrid.
                                              GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQWVCPAGAGTLEPGAPGSCYLDAGLRR
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hair loss; gene therapy.
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Length 1182;
                                                  IndelB
  Score 3682; DB 6;
Pred. No. 1.5e-296;
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99.4%;
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                          Best Local Similarity 99.4
Matches 689; Conservative
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The invention relates to a human hairless (HR) polynucleotide encoding the hairless (Hr) polypeptide. The invention also relates to an expression expression system compitation an expression construct which produces a polypeptide with hairless transcription factor activity, a reporter construct comprising a transcription factor activity, a reporter construct comprising a transcription regulatory region responsive to hairless transcription activity to regulate transcription of the reporter gene which is mediated by the transcription regulatory region and methods of screening for chemical agents which modulate hairless-mediated transcription, binding between hairless and thyroid hormone receptor or hairless activity. The polynucleotide is useful as a probe or primer to quantitate cognate RNA and DNA within cells, which can be subsequently used to correlate hair growth or loss with hairless expression or hairless-regulated transcription. The amino acid sequence of hairless antigen can be used for preparing specific binding molecules (e.g. polyclonal or monoclonal antibodies) for monitoring protein expression, confernity purification and for functional studies. The human hairless columnan-rodent somatic cell hybrids, and as an affinity tag to identify, isolate and detect interacting proteins that bind the hairless channer or protein. This sequence represents a rat hairless polypeptide of
                         1115 RLREEWGYSCWTLLQAPGEAVLVPAGAPHQYQGLVSTISVTQHFLSPETSALSAQLCHQG 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Hairless polypeptide and polynucleotide, useful for identifying and detecting this genetic marker in family pedigrees or human-rodent somatic cell hybrids, or detecting interacting proteins that bind hairless gene
RLREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLCHQG
                                                                                                                                                                                                                                                                                                                                                                                     Rat; hairless; Hr; thyroid hormone receptor; hair growth; hair loss; family pedigree; radiation hybrid; somatic cell hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 1207;
                                                                                                   ASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.8%; Score 3510;
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                                                                                                                                                                                                                           ABU62543 standard; protein; 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CARN-) CARNEGIE INST WASHINGTON.
                                                                                                                                                                                                                                                                                                                                             Rat Hairless (Hr) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example, Fig 1; 34pp; English.
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                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                           The invention relates to human Hairless (Hr) polypeptides and nucleic acid molecules (HR) encoding such polypeptides. The invention also relates to the Hairless expression constructs which may be used in transcription assays. Sequences of the invention are used in diagnosis and treatment of dermatological conditions such as hair loss. They are also used in gene therapy. Polymucleotides of the invention can be used as probes for the detection of hair loss. The present sequence is rat Hairless protein (Hr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGFRLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQTLTALGPPQPTSLDSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLDSTA
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                                                                                                                                                                                                                                              Novel expression construct, useful in the diagnosis and treatment dermatological conditions, such as hair loss, contains a Hairless
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; Pred. No. 3.2e-282;
11; Mismatches 21;
                                                                                                                        (CARN-) CARNEGIE INST WASHINGTON
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                                          99US-00287354.
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Best Local Similarity 95.1%
Matches 659; Conservative
                                                                                                                                                                                                        WPI; 2002-204622/26.
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                                            07-APR-1999;
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    19-FEB-2002
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                                  AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC
                                                                    AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC
                                                                                            SHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAELS
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                                                                                                                              TVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIKE
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                         VTQCQSCVQAAGEVGVLTGHSQKSRRSPLEEKQLEEEDSSATSEEGGGGPGPEASLNKGL
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No. 3.2e-282;
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hair loss; gene
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                                                                                                                                                                                                                                  of
gene
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                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to human Hairless (Hr) polypeptides and nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD
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                                                                                                                                                                                                                               Novel expression construct, useful in the diagnosis and treatment dermatological conditions, such as hair loss, contains a Hairless
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                                                   CARNEGIE INST WASHINGTON
                                                                                                                                                                                                                                                                                                                                                Example; Fig 1; 48pp; English.
98US-0080888P
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494 LAQCQSCAQAAGEGGGHACHSQQVRRSPLGGELQQEEDTATNSSSEEGPGSGPDSRLSTG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a human hairless (HR) polynucleotide encoding the hairless (Hr) polypeptide. The invention also relates to an expression system comprising an expression construct which produces a polypeptide with hairless transcription factor activity, a reporter construct comprising a transcription factor activity, a reporter construct comprising a transcription factor activity a reporter construct comprising a transcription regulatory region and methods construct comprising activity to regulatory region and methods construct binding between hairless and thyroid hormone receptor or hairless activity. The polynucleotide is useful as a probe or primer to quantitate cognate RNA and DNA within cells, which can be subsequently consed to correlate hair growth or loss with hairless expression or hairless regulated transcription. The amino acid sequence of hairless antigen can be used for preparing specific binding molecules (e.g. antigen can be used for preparing specific binding molecules (e.g. colyclonal or monoclonal antibodies) for monitoring protein expression, cor affinity purification and for functional studies. The human hairless coldentify and detect this genetic marker in family pedigrees, radiation chybrids or human-rodent sommatic cell hybrids, and as an affinity tag to dence the protein that bind the hairless construction. This sequence represents a human hairless polypeptide of the protein that the hairless construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Hairless polypeptide and polynucleotide, useful for identifying and detecting this genetic marker in family pedigrees or human-rodent somatic cell hybrids, or detecting interacting proteins that bind hairless gene
                                                                                                                                                                                                                                          Human, hairless; Hr; thyroid hormone receptor; hair growth; hair loss; family pedigree; radiation hybrid; somatic cell hybrid.
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                     HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 83.6%; Score 3095.5; DB 6, Local Similarity 83.2%; Pred. No. 9.5e-248; nes 579; Conservative 40; Mismatches 74;
                                                                                                                  ABU62542 standard; protein; 1189 AA
                                                                                                                                                                                                              Human Hairless (Hr) polypeptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CARN-) CARNEGIE INST WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 1; 34pp; English.
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                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                            Homo sapiens
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07-APR-1999;
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- PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRRRIREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLC 657
                 CSHCSHRLCVACGRIAGAGKONREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAEL 179
                                                                                                                    STVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIK 239
                                                                                                                                      793
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                                                                                                                                                                                                                                                                                                                                                                            YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD 537
LAKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWR 119
                                                                                                                                                                                                                                         TNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPR- 358
                                                                          CPRCSHRLCVACGRVAGTGRAREKAGFQEQSAEECTQEAGHAACSLMLTQFVSSQALAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                      alopecia; congenital alopecia; congenital atrichia; androgenetic alopecia; alopecia areata; alopecia mutant; hair follicle.
                                                                                                                                                                              EETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRI
                                                                                                                                                                                                                                                                                                                                                             STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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/noce= "Wild-type Thr substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Hairless mutant amino acid sequence, Thr (1022) Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY15218 standard; protein; 1189 AA.
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This is the amino acid sequence for the wildtype human hairless protein. The gene was discovered by genotryping a Paristani kindred (comprising of a ffected males and 7 affected females) with an inherited form of congenital alopecia universalis. The pedigree is strongly suggestive of autosomal recessive inheritance. The invention provides methods and sequences for the recombinant production of wild-type human hairless, mutant human hairless and wild-type human of winged-helix-nude) proteins, assays for screening for binding compounds, modulators and homoloques, and animal models of hairlessenses. Human hairless conditions such as androgenetic alopecia (male pattern baldness), alopecia areata, alopecia totalis, congenital alopecia universalis, congenital alopecia and severe T-cell immunodeficiency can be treated with compounds identified in the assays. The methods are also useful for identifying compounds that can be used to inhibit hair growth
                                                                                                                                                                                                                                                                                                                                                                           alopecia, congenital alopecia; congenital atrichia; androgenetic alopecia; alopecia areata; alopecia universalis; wildtype;
                                                                        1 VTQCQSCVQAAGEVGVLTGHSQKSRRSPL-EEKQLEEEDSSATSEEGGGGPGPEASLNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hairless gene and protein, useful for identifying modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 1189;
                                                                                                                                                                                                                                                                                                                                             Human Hairless wildtype protein amino acid sequence.
                                                                                                                                      658 HOGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
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83.0%; Pred. No. 3e-247;
iive 40; Mismatches 75;
                                                                                                                                                                                                                                         AAY15217 standard; protein; 1189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0073043P.
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                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 578; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ06349.
                                                                                                                                                                                                                                                                                                                                                                                                                  hair follicle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hair growth.
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                                                                                                                                                                                                                               This is the amino acid sequence for the mutant human hairless protein, which has Alanine substituted for Threonine at position 1022. The gene was discovered by genotyping a Pakistani kindred (comprising of 4 affected males and 7 affected feamles) with an inherited form of congenital alopecia universalis. The pedigree is strongly suggestive of autosomal recessive inheritance. The invention provides methods and sequences for the recombinant production of wild-type human hairless, mothlators and sequences for screening for binding compounds, modulators and homologues, and animal models of hairlessness. Human hairless conditions such as androgenetic alopecia (male pattern baldness), alopecia areata, alopecia totalis, congenital alopecia universalis, congenital alopecia and severe T-cell immunodeficiency can be treated with compounds and severe T-cell immunodeficiency can be treated with compounds compounds that can be used to inhibit hair growth
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    PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD

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                                                                                                                                                    hairless gene and protein, useful for identifying modulators
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.5%; Score 3093.5; DB 2
83.2%; Pred. No. 1.4e-247;
ive 40; Mismatches 74;
                                                 (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                        Claim 8; Page; 127pp; English.
                     98US-0073043P.
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                                                                                                                      WPI; 1999-479184/40.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1189 AA;
                                                                                     Christiano AM
                   29-JAN-1998;
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The invention discloses a new catalytic DNA or RNA molecule that

specifically cleaves, or inhibits expression of, Hairless Protein mRNA
which comprises a catalytic domain that cleaves mRNA at a defined

consensus sequence and binding domains contiguous with the 5' and 3' ends

consensus sequence and binding domains contiguous with the 5' and 3'

consensus sequence and binding domains contiguous with the 5' and 3'

confidence and binding domains contiguous of hair, known as

a trichia. Abundant hair growth, hirsutism, can be improved by inhibiting

the genes promoting hair growth, and one way to get targeted, transient

continuing ribozymes and DNAzymes. Ribozymes are RNA structures which have

concluding ribozymes and DNAzymes. Ribozymes are RNA structures which have

continuing ribozymes and DNAzymes. Ribozymes are RNA structure to the

hammerhead ribozyme, called deoxy-ribozymes on DNAzymes, having a

cotallytic core and two sequence specific arms. The deoxy-ribozymes have

cotallytic core and two sequence specific arms. The deoxy-ribozymes have

cotallytic core and two sequence specific arms. The deoxy-ribozymes have

cotallytic core and two sequence specific arms. The deoxy-ribozymes have

cotallytic core and two sequence specific arms. The deoxy-ribozymes have

cotallytic ore and two sequence specific arms. The deoxy-ribozymes have

cotally a hair-producing cell, for inhibiting hair growth and for inhibiting

cotal by a hair-producing cell, for inhibiting hair growth and for inhibiting

the transition of a hair follicle from the anagen phase to the catagen

cotal removal products which function by inhibiting hairless protein

cotal removal products which function by inhibiting hairless protein

cotal removal products which function by inhibiting hairless protein
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                                                                                                                                                                                                                                     New catalytic nucleic acid molecule that specifically cleaves Hairless Protein mRNA, useful for inhibiting hair production by a hair-producing cell, or for inhibiting transition of a hair follicle from anagen phase
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83.4%; Score 3089.5; DB 6; Length
Best Local Similarity 83.0%; Pred. No. 3e-247;
Matches 578; Conservative 40; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 59-63; 65pp; English.
                                                                                               COLUMBIA NEW YORK
                 12-APR-2002; 2002WO-US011683
                                                         13-APR-2001; 2001US-0283618P
                                                                                                                                                                              WPI; 2003-093020/08.
N-PSDB; ABX13987.
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359 -PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD 417
  relates to the Hairless expression constructs which may be used in transcription assays. Sequences of the invention are used in diagnosis and treatment of dermatological conditions such as hair loss. They are also used in gene therapy. Polynucleotides of the invention can be used as probes for the detection of hair loss. The present sequence is human Hairless protein (Hr)
                                                                                                                                                                                                                                                                                             STAMHQVWVKFDIRGHCPCQADARVWAPGDAGQQKESTQKTPPTPQPSCNGDTHRTKSIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; hairless; Hr; thyroid hormone receptor; hair growth; hair loss;
                                                                                                                                                                                                                                                CPRCSHRLCVACGRVAGTGRAREKAGFQEQSAEECTQEAGHAACSLMLTQFVSSQALAEL
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                                                                                                    984;
                                                                                                    Length
                                                                                                                          Indels
                                                                                                 83.4%; Score 3088.5; DB 5;
83.0%; Pred. No. 2.8e-247;
iive 40; Mismatches 75;
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                                                                              Sequence 984 AA;
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                                                                                         FLSGLDGEGLWSPGSQVSTVWHVFRAQDAQRIRRFLQWVCPAGAGALEPGAPGSCYLDAG
                                                                           YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD
                                                                                                                       FLSGLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAG
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NO:1 (AAD31072)
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NO:1 (AAD31077)
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NO:1 (AAD31077)
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hair loss; gene
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protein, Hr protein, HR gene, dermatological condition, therapy, single zinc finger transcription factor protein.
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EETPDSAETPAEDRAGRGPLPCPSLCELLASTAVKLCLGHERIHMAFAPVTPALPSDDRI
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hair loss; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Hairless polypeptide and polynucleotide, useful for identifying and detecting this genetic marker in family pedigrees or human-rodent somatic cell hybrids, or detecting interacting proteins that bind hairless gene
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83.4%; Score 3088.5; DB 6; Length 984;
Best Local Similarity 83.0%; Pred. No. 2.8e-247;
Matches 578; Conservative 40; Mismatches 75; Indels 3;
             family pedigree; radiation hybrid; somatic cell hybrid.
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                                                                                                                                                                                                                                                                               21-DEC-2001; 2001US-00024368
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                                                                                     Homo sapiens.
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07-APR-1999;
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07-APR-1999;
            06-FEB-2003
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                                                                                                                                                                                                                                                                                  1 VTQCQSCVQAAGEVGVLTGHSQKSRRSPL-EEKQLEEEDSSATSEEGGGGPGPEASLAKG
                                                                                                               LAKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWR
                                                                                                                           CSHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVBSQALAEL
                                                                                                                                                                CPRCSHRLCVACGRVAGTGRAREKAGFQEQSAEECTQEAGHAACSLMLTQFVSSQALAEL
                                                                                                                                                                                           STVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIK
                                                                                                                                                                                                                                           TNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPR-
                                                                                                                                                                                                                                                                                                             - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
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                                                         Gaps
putative single zinc finger transcription factor protein (Hairless)
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                                       Length 1189;
                                     83.1%; Score 3077.5; DB 5; Length
82.9%; Pred. No. 3e-246;
ive 37; Mismatches 79; Indels
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                                 Query Match
Best Local Similarity 82.9<sup>5</sup>
Matches 577, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                   Sequence 1189 AA;
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The invention relates to a human hairless (HR) polynucleotide encoding the hairless (Hr) polypeptide. The invention also relates to an expression system compitating an expression construct which produces a polypeptide with hairless transcription factor activity, a reporter construct comprising a transcription factor activity, a reporter construct comprising a transcription regulatory region responsive to hairless transcription activity to regulatory region responsive to gene which is mediated by the transcription regulatory region and methods of screening for chemical agents which modulate hairless-mediated cranscription, binding between hairless and thyroid hormone receptor or hairless activity. The polynucleotide is useful as a probe or primer to cused to correlate hair growth or loss with hairless expression or hairless regulated transcription. The amino acid sequence of hairless antigen can be used for preparing specific binding molecules (e.g. colynucleotide, polypeptide or specific binding molecules (e.g. colynucleotide, polypeptide or specific binding molecule may be used to dentify and detect this genetic marker in family pedigrees, radiation hybrids or human-rodent somatic cell hybrids, and as an affinity tas to content or procein. This sequence represents a human hairless polypeptide of interacting proteins that bind the hairless contents and detect interacting a human hairless polypeptide of the represents a human hairless polypeptide of the represents a human hairless polypeptide of the represents and mental human hairless polypeptide of the represents and human hairless polypeptide of the represents and human hairless polypeptide of the represents and human hairless beliable to the represents and human hairless beliable to the represents and human hairless beliable to the represents and human hairless the hairless that human hairless the human hairless the human hairless the human hairless the human hairless the human hairless the human hairless the human hairless the human hairless the human hairl
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82.9%; Pred. No. 3e-246;
Live 37; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                 (CARN-) CARNEGIE INST WASHINGTON
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                                                                                                                    98US-0080888P.
99US-00287354.
21-DEC-2001; 2001US-00024368.
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Matches 577; Conservative
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WPI; 2003-492034/58
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                                                                                  N-PSDB; ACD26351
                            07-APR-1998;
07-APR-1999;
                                                               Тһотрвоп СС;
06-FEB-2003
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        - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
               STTFWEGFSWPELRPKSDEGSVLLLHRAFGDEDTSRVENLAASLPLPEYCALHGKLNLAS
                                                               YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD
                                                                                           FLSGLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAG
                                                                                                                      LRRRIREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLC
                                    STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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/note= "Encoded by
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The invention relates to a human hairless (HR) polynucleotide encoding the hairless (Hr) polypeptide. The invention also relates to an expression construct which produces a polypeptide with hairless transcription factor activity, a reporter construct comprising a transcription regulatory region responsive to hairless transcription activity to regulatory region responsive to careful as mediated by the transcription regulatory region and methods of screening for chemical agents which modulate hairless-mediated receptor transcription, binding between hairless and thyroid hormone receptor or hairless activity. The polynucleotide is useful as a probe or primer to quantitate cognate RNA and DNA within cells, which can be subsequently used to correlate hair growth or loss with hairless expression or hairless-regulated transcription. The amino acid sequence of hairless antigen can be used for preparing specific binding molecules (e.g. polyclonal or monoclonal antibodies) for monitoring protein expression, for affinity purification and for functional studies. The human hairless polynucleotide, polypeptide or specific binding molecule may be used to identify, isolate and detect interacting proteins waiting to human-roadent sommatic cell hybrids, and as an affinity tag to identify, isolate and detect interacting proteins that bind the hairless gene or protein. This sequence represents a human hairless polypeptide of
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82.0%; Pred. No. 1.5e-245;
:ive 47; Mismatches 75;
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99US-00287354.
21-DEC-2001; 2001US-00024368
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les 571; Conservative
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Search completed: November 25, 2005, 22:06:40 Job time : 196 secs



12404, A 3398, Ap 2, Appli 6, Appli 23771, A 32740, A

10, Appl 2, Appli 2, Appli 10703, A 2, Appli 2, Appli 11117, A 38, Appl

sequence 2, sequence 327 sequence 327 sequence 327 sequence 327 sequence 2, sequence 2, sequence 2, sequence 2, sequence 38, sequence 3

9845, Ap 2514, Ap

Perfect score:

6

Run

Sequence:

Scoring table:

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Database

Searched:

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490 VTQCQSCVQAAGEVGVLTGHSQKSRRSPLEEKQLEEEDSSATSEEGGGGGPGPEASLNKGL 549
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Sequence 6, Application US/09287354

Patent No. 6348348

GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
FILE REFERENCE: Thompson-20263/0243435

CURRENT APPLICATION NUMBER: US/09/287,354

CURRENT FILING DATE: 1999-04-07

RABLIER PILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 10

SOFFWARE: Patentin Ver. 2.0
        US-10-104-047-3398

US-09-466-778-2

US-09-079-4318-6

US-09-252-991A-32778

US-09-252-991A-32778

US-09-252-991A-32778

US-09-69-005A-10

US-09-699-115-2

US-09-699-115-2

US-09-949-016-10703

US-09-949-016-10703

US-09-949-016-1117

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US-09-949-016-1117

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US-09-949-016-9485

US-09-605-703B-2514
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99.4%; Score 3682; D
Best Local Similarity 99.4%; Pred. No. 0;
Matches 689; Conservative 1; Mismatches
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TYPE: PRT
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Sequence 6931, Ap
Sequence 2, Appli
Sequence 3, Appli
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Sequence 1138, Ap
Sequence 10, Appl
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1193.630 Million cell updates/sec
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Sequence 5,
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3704
1 VTQCQSCVQAAGEVGVLTGH.......MDRAVFQAVKAAVGALQEAK
                                                                                             November 25, 2005, 22:00:26; Search time 48 Seconds
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-538-092-1289
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Listing first 45 summaries
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                                                LGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLS
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83.2%; Pred. No. 1.7e-282;
iive 40; Mismatches 74;
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09287354
Fatent No. 6348348
GENERAL INFORMATION:
APPLICANT: THOMPSON, Catherine C.
TILLE OF INVENTION: HUMAN HAIRLESS GENE AND FILE REFERENCE: Thompson-20263/0243435
CURRENT APPLICATION NUMBER: US/09/287,354
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: US 60/080,888
SEARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 579; Conserv
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    HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQTLTALGPPQPTNLDSTA
                                                  FWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLASSLPLPEYCAHQGKLNLASYLP
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Patent No. 6348348

GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
FILE REPERRENCE: Thompson-20263/024335
CURRENT APPLICATION NUMBER: US/09/287,354
CURRENT FILING DATE: 1999-04-07

EARLIER APPLICATION NUMBER: US 60/080,888

EARLIER APPLICATION NUMBER: US 60/080,888

EARLIER APPLICATION NUMBER: US 60/080,888

EARLIER APPLICATION NUMBER: US 60/080,888

EARLIER PILING DATE: 1999-04-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 1207
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854 CPRRGFHLFQEHWRQGQPVLVSGIQRTLQGNLWGTEALGALGGQVQALSPLGPPQPSSLG
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Patent No. 6348348

GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/287,354

CURRENT FILING DATE: 1999-04-07

EARLIER FILING DATE: 1998-04-07

SERIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
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CORGANISM: Homo sapiens
US-09-287-354-2
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Sequence 6931, Application US/09949016

Patent No. 6812339

GENERAL INNEMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE REPERENCE: CLO01307

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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                                                                                      478 YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD
CPRRGFHLFQEHWRQGQPVLVSG1QRTLQGNLWGTEALGALGGQVQALSPLGPPQPSSLG
                             STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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83.2%; Pred. No. 1.7e-282;
live 40; Mismatches 74; I
                                                                                                                                                                                                                                                                                                  658 HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
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Best Local Similarity 83.2*
Matches 579; Conservative
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; ORGANISM: Human
US-09-949-016-6931
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US-00-949-016-7891

Sequence 7891. Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT PAPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEG ID NO 7891
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387 TAEQGAGGWQEVRDTSIG-NKDVDSGQHD-------EQKGQGPAVTEDSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            490 ACSLMLTQFVSSQALAELSTAMHQVWVKFDIRGHCPCQADARVWAPGDAGQQKESTQKTP
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                                            - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
                                                                                                  STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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                                                                                                                                                                                                                                                                                                                                          63.0%; Score 2333.5; DB 2; 77.2%; Pred. No. 9.4e-211; ive 35; Mismatches 63;
                                                                                                                                                                                                                                                                                                                              HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
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438; Conserv
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Best Local S
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                                                                                                                                                           537
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    STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
                                                                                                                                                           YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: THOMPSON, Catherine C.
TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
FILE REFERENCE: Thompson-20263/0243435
CURRENT APPLICATION NUMBER: US/09/287,354
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: US 60/080,888
EARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                               HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09287354; Patent No. 6348348; GENERAL INFORMATION:
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Best Local Similarity 82.9
Matches 577; Conservative
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1793 PŚCÓKMKRV--VQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHKL 1850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003 PRPNQVSGPVMPSM-PPGQ--WQQAPLP-------QQQP--MPGLPR----PVIS 2041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GRIAGAGKNREKTGSQEQHTDDCAQEAGHAA-----CSLILTQF 170
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                                                                                                                                                                                                                                                                                                                                                                                      Indels 317;
                                                                                                                                                                                                                         Length 2442;
                                                                                                                                                                                                                       Query Match
4.1%; Score 152.5; DB 2;
Best Local Similarity 18.2%; Pred. No. 0.00024;
Matches 156; Conservative 104; Mismatches 282;
PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 10
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                                                                                                                                            TYPE: PRT
ORGANISM: human
                                                                                                                                                                                    US-09-514-247A-10
                                                                                                                         LENGTH: 2442
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Sequence 10, Application US/09514247A

Sequence 10, Application US/09514247A

Sequence 10, Application GES5361

APPLICANT: TANGUCHI, Tomoyasu

APPLICANT: TANGUCHI, Tomoyasu

APPLICANT: MIZUKAMI, JUNKO

TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTACONIST TO IS
FILE REPRENCE: TANGUCHI=6

CURRENT APPLICATION NUMBER: US/09/514,247A

CURRENT FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: PCT/JP98/03734
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  IHMAFAPVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPV
                    RTRLSPPGALLWLQEPR--PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLG
                                                                                                      GOVOSLTALGPPOPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDAS-----
                                                                                                                                                                               ----RVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHPLEPQLWAAYGVNSHRGHLGT
                                                                                                                                                                                                                                                                     790 TPYPDRVENLAASLPLPEYCALHGKLNLASYLPPGLALRPLEPQLWAAYGVSPHRGHLGT
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APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.10211U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            594
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Patent No. 6833446
GENERAL INFORMATION:
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US-09-640-211A-1138
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               --KLNLASYLPLGLTLHPLEPQLW 493
                                                                                                                                                                                                                                                         2218 SAGMAGHGOFQOPQGPGGYPPAM-----QQQQRMQQHLPLQGSSMGQMAAQMGQL
                                                                                                                                                                                                         538 ---FLSGLDGEGLW----SPGSQTSTVWHVFRAQDAQRIRRFL------QMVCPAG--
                                                                                                                                                                                                                                                                                                         --AGTLEPGAPGSCYLDAGLRRRLREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTI
                                                                                                              SHRGHLGTKNLCVEVSDLI --SILVHAEAQLPPWYRAQKD---
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APPLICANT: Ewen, Mark
APPLICANT: Ewen, Mark
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 1944
CLASSIFICATION: 436
ATTONER/AGART INFORMATION:
NAME: Williams Ph. D. Kathleen A.
REGISTRATION NUMBER: 34,380
REFRENCE/DOCKET NUMBER: 34,380
REFRENCE/DOCKET NUMBER: 36,380
TELEBHOMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBHOME: (617) 542-2290
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARACTERISTICS:
LENGTH: 244 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.0%; Score 146.5; DB 1;
Best Local Similarity 19.0%; Pred. No. 0.00089;
Matches 141; Conservative 70; Mismatches 242;
                      445 TLGDKDASRVQNLVSSLPLPEYCAHQG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08227536 Patent No. 5658784 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           639 SVTQHFLS--PETSALSAQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GRIAGAGKNREKTGSQEQHTDDCAQEAGHAA-----CSLILTQF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- PIEKTP--PTPQPSCNGDS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 NRTKDIKEETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPA 292
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                                                                                                            Sequence 1370, Application US/09538092
| Sequence 1370, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Glot. Loic
| APPLICANT: Mansfield, Traci A. |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION NUMBER: US/09/538,092 |
| CURRENT FILING DATE: 1999-04-01/27,352 |
| PRIOR FILING DATE: 1999-04-01 |
| PRIOR FILING DATE: 1999-04-01 |
| PRIOR FILING DATE: 2000-02-01 |
| NUMBER OF SEQ ID NOS: 1387 |
| SSQ ID NO 1370 |
| LENGTH: 2442 |
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4.1%; Score 152.5; DB 2; Length 2442;
Best Local Similarity 18.2%; Pred. No. 0.00024;
Matches 156; Conservative 104; Mismatches 282; Indels 317; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q92793
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2315 SPQQHMLSGQPQASHLPGQ 2333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-538-092-1370
                                                                                             -09-538-092-1370
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1632 TLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDRFVYTCNECKHHV-ETRWHCTVCEDYD 1690
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|LCITCYNTKNHDHKMEKLGLGLDDESNNQQAAATQSPGDSRRLSIQRCIQSLVHACQCRN 1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||| || || : || || : || || 2070 VLSIL-HANPQLLAAFIKQRAAKYANSNPQPIPGQPGMPQGQPGLQPTM----PGQGGV 2124
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                                                                                                                                                                                                                                -----HCCSRCHHGLFNTHWRCSHC-SHR 126
                                                                                                                                                                                                                                                                                                                                                                       LCVACGRIAGAGKNREKTG----- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 -- CSLILTQFVSSQALAELSTVMHQAWAKFDIRGHC-------FCQVD---- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 SCNGDSNRTKDIKEETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAF 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 APVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLS 346
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                                                                                  Indels 289;
                                              Length 2414;
                                                                                                                                                                                                        --HLLSGLGDRLCRLLRKEREALAWAQREGQGPA-----MTEDSPGIP---
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GENERAL INPRMATION:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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STREET: Ten Post Office Square
                                        4.0%; Score 146.5; DB 2;
19.0%; Pred. No. 0.00089;
rative 70; Mismatches 242;
                                                                                                                        29 LEE--KQLEEEDSSATSEEGGGGPGPE-----
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                                          Query Match
Best Local Similarity
Matches 141; Conserv
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STATE: MA
COUNTRY: US
  US-09-538-092-1289
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TLARDKHLEFSSLRRAQWSTMCMLVELHTQSQDRFVYTCNECKHHV-ETRWHCTVCEDYD 1690
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                                                                                                                                           -----SQEQHTDDCAQEAGHAA---- 162
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Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Glot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-54

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURAPARSESGFFORMATHER VERSION 0.9

SOFTWARE: CURAPARSESGFFORMATHER VERSION 0.9
                                                                                                                                                                                                                         --CSLILTQFVSSQALAELSTVMHQAWAKFDIRGHC---------FCQVD----
                                                                                                                                                                                                                                                                                                          --ARVWAPGDGGQQK---EPTEKTPPTP---QP
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                                                               NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q09472
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NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9672
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                                                                                                                                                568 RIRRFLOMVCPAGAGTLEPGAP 589
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (619)-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 158; Conserva
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US-08-194-468-2
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COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
FLING DATE:
FLING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-April-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 146.5; DB 4; Best Local Similarity 19.0%; Pred. No. 0.00089; Matches 141; Conservative 70; Mismatches 242;
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                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-308Xq999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 451-0313
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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Sequence 2, Application US/08194468
Patent No. 5750336
GENERAL INFORMATION:
APPLICANT: MONITUMIN, MAIC R.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF TITLE OF INVENTION: RESPONSIVE GENES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
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2070 VLSIL-HANPQLLAAFIKQRAAKYANSNPQPIPGQPGMPQGQPGLQPPTM----PGQQGV 2124
461 LPLP---EYCAHOGKLNLASYLPLG-LTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSD 516
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444 South Flower Street, Suite 2000
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APPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FEB-1994
TIGNETION: 435
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3.9%; Score 145.5; DB 2; Length 2441;
Best Local Similarity 18.6%; Pred. No. 0.0011;
Matches 158; Conservative 101; Mismatches 290; Indels 301; Gaps
                                                                                                                                                       1851 VROQQIQHCLQQAQLMRRRMATMNTRNVPQQSLPSPTSAPPGTPTQQPS-----
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TITLE OF INVENTION: Methods for Treating Diabetes Mellitus FILE REPRENCE: SALK1650-1
CURRENT APPLICATION NUMBER: US/08/961,739A
CURRENT FILING DATE: 1997-10-31
EARLIER APPLICATION NUMBER: US 194,468
EARLIER APPLICATION NUMBER: US 194,468
EARLIER PILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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Patent No. 6063583
GENERAL INFORMATION:
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; OTHER INFORMATION: Xaa
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.679 FSSLRRSKWSTLCMLVELHTQGQDRFVYTCNECKHHV-ETRWHCTVCEDYDLCINCYNTK 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1794 -PSCOKMKRV--VQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHN 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1851 VRQQQIQHCLQQAQLMRRRMATMNTRNVPQQSLPSPTSAPPGTPTQQPS------ 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1957 VE-----AARQIEREAQQQQHLYRANINNGMPPG-RDGMGTPGSQMTPVGLNVPRPNQV 2009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1738 SHTHKMVKWGLGLDDEGSSQGEPQSKSPQESRRLSIQRCIQSLVHACQCRNANCSL---- 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2107 AKYVANQPGMQPQPGLQSQPGMQPQPGMHQQPSLQNLNAMQAGVPRPGVPPPQPAMGGLN 2166
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                                                                                                                                                                                                                                                                                                                                                                           ------GRIAGAGKNREKTGSQEQHTDDCAQEAGHAA-----CSLILTQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------QVDARVWA---PGDGGQQK--EPTEKTP--PTPQPSCNGDSNRTKDI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 ITNILDSIIAQVVERKIQEK-----317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 LGG----QVQSLTALGPPQPTNLDSTAFWEGFSHPETRPK---LDEGSVLLLHRTLGDKD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 ASRVQNLVSSLPLPEYCAHQG------KLNLASYLPLGLTLHPLEPQLWAAYGVN 499
                                                                                                                                                                                                                                         -----SHRGH-LGTKNLCVEVSDLI--SILVHAEAQLPPWYRAQK-----DFLSGLD 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 APGSCYLDAGLRRRLREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLS- 646
DRICKLIRKEREALAWAQREGOGPAMTEDSPGIP-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 KEETPDSTESPARDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 LSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGT
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916, App 62, Appli 1129, Ap 10, Appl 28, Appl 28, Appl 1523, Ap 4, Appli 1040, Appl

54, Appl 41, Appl 1219, Ap

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Sequence 1477, Application US/10821234
; Sequence 1477, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Turbar
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT APPLICATION NUMBER: US 60/462,047
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GPPADSSKPIGPDDAIDALSSDF-----TCGSPTAAGKKTEKEESTEVLK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 IDTLGGPEETEEENTTYTGPEVS--DPMSSTYIEELGKREVTIPPKYRELL--AKKEGIT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 GPAMTEDSPGIPHCCSRCHHGLFNTHWRCSHCSHRLCVACGRIAGAGKNREKTGSQEQHT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 DDCAQEAGHAACSL-----ILTQFVSSQALAELSTVM--HQAWAKFDIRGHCFCQVD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKAKEEKLEKCGEDDETIPSEYRLKPATDKDGKPLLPEPEEKPKPRSESELIDELSEDF 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 DIKE--ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPA-- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TSEEGGGGPGPEASLNKGLAKHLLSGLGDRLCRLLRKEREALAWAQREG-Q 91
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3.1%; Score 115; DB 1; Length 667;
Best Local Similarity 20.4%; Pred. No. 0.046;
Matches 112; Conservative 55; Mismatches 191; Indels 192;
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US-10-967-527A-16
US-10-821-234-1657
US-10-982-545-6
US-10-131-826A-50
US-10-131-826A-30
US-10-131-826A-346
US-10-821-234-916
US-11-150-406-2
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US-11-045-802-26
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US-11-045-802-26
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US-11-045-802-26
US-11-045-802-26
US-11-057-058-10
US-11-057-058-10
US-11-057-058-11
US-11-057-058-11
US-11-057-058-11
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    LENGTH: 667
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Sequence 1155, Ap
Sequence 9, Appli
Sequence 6, Appli
Sequence 1514, Ap
Sequence 1658, Ap
Sequence 1658, Ap
Sequence 1556, Ap
Sequence 28, Appli
Sequence 38, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
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Sequence 36, Appl
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Sequence 36, Appl
Sequence 36, Appl
Sequence 40, Appl
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Sequence 2, Appli
Sequence 14, Appl
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Sequence 1, Appli
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Sequence 921, App
Sequence 20, Appl
                                                                                               November 25, 2005, 22:06:54; Search time 10 Seconds (without alignments) 210.046 Million cell updates/sec
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                                                                                                                                                        US-10-712-629B-18
3704
1 VTQCQSCVQAAGEVGVLTGH......MDRAVFQAVKAAVGALQEAK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA New:*

1: /cgn2_6/ptodata//pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US1_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US1_NEW_PUB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-971-982-2
US-10-821-234-921
US-11-015-546A-20
US-10-131-56A-412
US-10-131-286A-412
US-10-131-286A-438
US-10-821-234-1556
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US-11-135-855-39
US-10-821-234-1126
US-11-059-982-1
                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                             17545 segs, 3030971 residues
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                    Run on
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25;

Gaps

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969 QQQQQQQQQQQQQQQMLQMRTGE-----IPMGWGVNPYSPAVQSNQPG 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                            1016 SWPEGMLSMEQGPHGSQNRPLIRNSLDDLLGPPSNAEGQSDE--RALLDQLHTFLSNTDA 1073
                                                                                                                                                          493 -WAAYGVNSHRGHLGTKN---LCVEVSDLISILVHAEAQLPPWYRAQKD----FLSGLDG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRCS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 IIAMSTIFI--MAIAIVLIIMFYILKTKPSAPACCTSHPGKSVEAQVSKDEEKKEAPDNV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 ----QKEPTEK---TPPTPQPSCNGDSNRTKDIKEETPDSTESPAEDGAGRSPLPCPSLC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 VMFSEKDEFEKLTATPAKPTKSENDASSENEQLLSRSVDSDEEPAPDKQG-----SPELC 301
                                                                                                                                                                                                                         384 TLRLSLWGMEALGTL-----GGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGS 438
                                                                                                                                                                                                                                                                   930 T-----GADYSATLPRPAMGGSVPTL----PLRSNRL-------PGARPSLQQQQ 968
                                                                                                                                                                                                                                                                                                                439 VLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHPLEPQL----- 492
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                                                                                 ----QPVQSVRPPYNRAVS-LDSPVSVGSGPPVKOVVSAFPGLPKQPILAGNPRMMDSQ 885
                                                                                                                                325 -RAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQK 383
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785 VS--GDLDNLDAILGDLTSSDFYNNPTNGGHPGAKQQMFAGPSSLGLRSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%; Score 101; DB 1; Length 447; Best Local Similarity 23.8%; Pred. No. 0.34; Matches 72; Conservative 31; Mismatches 119; Indels
                                            281 RIHMAFAPVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fox, Brian A.
APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zenfil4, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
FILE REPERSUES: 03-17
CURRENT APPLICATION NUMBER: US/10/967,527A
CURRENT FILING DATE: 2004-10-18
PRIOR FILING DATE: 2003-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1074 TGLEEIDRALGIPELVNQĞQALESKQDVFQGQEA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 EG-----LWSPGSQTSTVWHVFRAQDA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/10967527A; Publication No. US20050256041A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: homo sapiens
US-10-967-527A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALAWAQREGQGPAMTEDSPGIPHC--------CSRCHHGLFNTHW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GHSSLINSPLDPNCKDSSVSVTSPSGVSSSTSGTVSSTSNVHGSLLQEKH 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCSHCSHRLCVACGRIAGAGK-NREKTGSQEQHTDDCAQ------EAGHAACSL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R---ILHKILQNGNSPAEVAKITAEATGKDTSSTASCGEGTTRQEQLSPKKKENNALLRY 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 ILTQFVSSQALAELSTVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIDRDDPSDVLAK--ELQPQADSGDSKLSQCSCSTNP----SSGQEKDPKIKTETNDE 784
  | | | | : | : | : | | DRSECKEKPSKPTEKTEESKAAAAPAP---VSBAVCRTS--MC-----SIQSAPPEPATL 384
                                                                                                                                                          RTRLSPPGALLWLQEPRPKHG-----FHLFQEHWRQGQPVLVSGIQKTLRLSLWGM 392
                                                                                                                                                                                                    ------KEEDREKLGEKEETIPPDYRLEEVKDKDGKPLLPKESKEQL----- 462
                                                                                                                                                                                                                                                   393 EALGTLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPYLLDEGSVLLLHRTLGDKDAS 452
                                                                                                                                                                                                                                                                                             ---LPSDDRITNILDSI-----IAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosenfeld, Michael G.
APPLICANT: Rose, Christopher K.
APPLICANT: Rose, David W.
APPLICANT: Rose, David W.
APPLICANT: Rose, David W.
TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
FILE REFERENCE: 627-PA1021
CURRENT APPLICATION NUMBER: US/10/971,982
CURRENT APPLICATION NUMBER: US/09/445,353
PRIOR FILING DATE: 2000-05-05
PRIOR PELICATION NUMBER: PCT/US98/12263
PRIOR FILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: 60/049,452
PRIOR FILING DATE: 1997-06-12
PRIOR PELING DATE: 1997-06-12
SPRIOR PELING DATE: 1997-06-12
SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKSRRSPLEEKQLEEEDSSATSEEGGGGPGPEASLNKGLAKHLLSGLGDRLCRLLRKERE
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19.4%; Pred. No. 1.2;
ive 75; Mismatches 242; Indels 194;
                                                                                                             385 KGTVP-DDAVEALADSLGKKEADPEDGKPVMDKVKEKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (3121)..(3121)
OTHER INFORMATION: "n" is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10971982
Publication No. US20050244889A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.4%
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                               AISEVVSQTP 506
                                                                                                                                                                                                                                                                                                                                            453 RVQNLVSSLP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402
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270 ASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGE 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 HHHHHANSVPLVP--------RGSREFGTAGSAWIPGGATARAEP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 TEXTPPTPQPSCNGDSNRTKDIKEETPD----STESPAEDGAG---RSPLPCPSLCELL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 DSPGIPHCCSRCHHGLFNTHWRCSHCSHRLCVACGRI-AGAGKNREKTGSQEQHTDDCAQ 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 IMPNIPQ------MSAFW-----YAVRTAVINAASGROTVDEALKDAQTNSSSH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 ar--pragaprtrgosgr-----eppgpaaatttpppggagsraraptpprapap 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 ASTAVKLCLGHDRIHMAFAPVTPA----LPSDDRITNILDSIIAQVVERKIQEKALGPGL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 A-----VLRRGGADGRAATALELPAPSGIGHVQTT----VLRRGGADGRAAAAL 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 ASLNKGLAKHLISG--LGDRLCRLIRKEREALAWAQRE----GQGPAMT-----E 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Artificial DNA sequence, polypeptide sequence of; OTHER INFORMATION: the MBP-ztnf13 fusion
US-11-015-546A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
2.6%; Score 97; DB 7; Length 614;
Best Local Similarity 22.8%; Pred. No. 1.1;
Matches 79; Conservative 27; Mismatches 138; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 RAGSGLRKGL----SLPLSPVRTRLSPPGALLWLQEPRPKHGFHL 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 RGAHGHARPLPQDRHALPESP-RORGEAGAASQLOAALPGPGLHL 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97; .DB 7; Length 614;
Pred. No. 1.1;
TITLE OF INVENTION: Ztnf13, A TUMOR NECROSIS FACTOR
                     FILE REPERENCE: 03-24
CURRENT APPLICATION NUMBER: US/11/015,546A
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 200
LENGTH: 614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 412, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stewart, Timothy A.
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, Victoria
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 WGMEALGTLGGQ-VQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGD 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 KDASRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHPLEPQLWAAYGVNSHRGHLGTK 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 N--LCVEVS---DLISILVHAEAQLPPWYRAQKDFLSGLDGEGLW-----SPGSQTS 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 TVWHVFRAQDAQRIRRFLQMVCPAGAGTL----EPGAPGSCYLDAGLRRRLREEWGV--- 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SCWTLLQAPGEAVLVPAGA-PHQVQGLVSTISVTQHFLSPETSALSAQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 -GAGRKLPDTGRCPVTE-----GSTVQLIAP--WNADVHSH----GDK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 P-----KTPEVTPLRLELQKL-PGLANTTLSTPNPDTQASASPDP----RPLREEEBARLL 234
                                                                                                                                                                                                                      Sequence 921, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Trang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICANTION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LEAALGLPVKKPRLRGPRPGSLTRLAB-------VSG----VSG-----
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2.6%; Score 97.5; DB 1; Length 658;
Best Local Similarity 22.9%; Pred. No. 1;
Matches 86; Conservative 32; Mismatches 124; Indels 13
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Publication No. US20050250126A1
GENERAL INFORMATION:
APPLICANT: GAO, ZEREN
APPLICANT: SHEPPARD, PAUL O.
APPLICANT: HOLLOWAY, JAMES L.
APPLICANT: APPLICANT: APPLICANT:
APPLICANT: APPLICANT: APPLEBY, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 921
LENGTH: 659
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; ORGANISM: Homo sapiens
US-10-821-234-921
                        EL 267
                                                                              302 LL 303
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US-11-015-546A-20
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1155
LENGTH: 4419
                                                                                                ; ORGANISM: Homo sapiens
US-10-821-234-1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- ONCSNYTVRFLCPPGSLR---RDTERIWSPWSPWSKCS----AACGOTGVOTRTRIC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 LAELSTVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAEMVSLCSEASEEGO---HCM-------GÓDCTACDLTCPMGÓVNADCDACMC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 KD---------IKEETPDSTESPAEDGAGRSPLPCPSLCELLASTAVK 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------PAPIVLTMPK----TSLKAATIKAEFVRAETPYMVMNPETKA---RRAG 323
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
RELOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQRPG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550 SEQ ID NO 412 LENGTH: 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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      PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR PLING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059112
PRIOR APPLICATION NUMBER: 60/05912
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
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US-10-131-826A-412
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2969 TLDLNCVVPGQAHAQVTWYKRGGSLPARHQTHGS-QLKLHHVSPADSGEYVCRAAGGPGP 3027
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                                                                                                                                                                                                                                                                                                                                                            269 ASTAVKLCLGHDRIHMAFAPVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 GLRKGLSLPLSPVRTRLSPPGALLWLQEPRP-KHGFHLFQEHWRQGQPVLVSGIQKTLRL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 SLWGMEALGTLG-----GQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 LLLHRTLGDKDASRVQNLVSSLPLPE---YCAHQGKLNLAS----YLPLGLTLHPLEPQ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548 WS-----PGSQT--STVWHVFRA--QDAQRIR-RFLQMV--CPAGAGTLEPGAPGSCYL 594
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                                                                                                                                                                                                                                          213 QKEP--TEKTPPTPQPSCNGDSNRTKD--IKEETPDSTESPAEDGAGRSPLPCPSLCELL 268
                                                             Gaps
                                                                                                                                                                                                                                                                                  Query Match 2.6%; Score 95; DB 1; Length 4419; Best Local Similarity 19.7%; Pred. No. 18; Matches 122; Conservative 61; Mismatches 206; Indels 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 -KNLCVEVSDL----ISILVHABAQLPPWYRAQKDFLSGLDGEGL-----
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US/10/186,643
PRIOR APPLICATION NUMBER: US/09/573,986
PRIOR FILING DATE: 2000-00-18
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; Publication No. US20050255100A1
; GENERAL INFORMATION:
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285 AFAPVTPALPSDDRITNILDSIIAQV-VERKIQEKALGPGLRAGSGLRKGLSLPLSPVRT 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 YYYG---DLYTBADLHR-----SVLCAPAGHLVFENDFSEFDSTQNNVSLDLECELMRRF 276
                                                                                                                                                                                                                                                                             344 RLSPPGALLWLQEPRPKHGFHLFQEHWRQG---QPVLVSGIQKTLRLSLWG----- 391
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                                                                                                                                                                                                                                                                                                            51 AINPPGPVL-------EQGLLYMPARLDGRDEVVKLQLSDTVHCRLAAP 92
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                                                                                                                                            Gaps
                                                                                        Query Match
2.5%; Score 93; DB 7; Length 483;
Best Local Similarity 22.7%; Pred. No. 1.6;
Matches 88; Conservative 39; Mismatches 120; Indels 140;
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                                                                                                                                                                                                                                                                                                                                                                     392 ---MEALGTLGGQVQSLTALGPPQPTNLDSTA-FWE--GFSHPET-----
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
                          ) ORGANISM: Hepatitis E virus US-11-184-574-4
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US-10-821-234-1514
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Best Local S
Matches 157
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    TYPE: PRT
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Publication NO. US20050255461A1
GENERAL INFORMATION:
APPLICANT: Meng, Xiang-Jin
APPLICANT: Haqshenas, Gholamreza
APPLICANT: Hadshenas, Gholamreza
TITLE OF INVENTION: AVIAN HEPATITIS-SPLENOMEGALY SYNDROME AND MAMALIAN
TITLE OF INVENTION: ABAINST AVIAN HEPATITIS-SPLENOMEGALY SYNDROME AND MAMALIAN
TITLE OF INVENTION: ABAINST AVIAN HEPATITIS E
TITLE OF INVENTION: AGAINST AVIAN HEPATITIS-SPLENOMEGALY SYNDROME AND MAMALIAN
TITLE OF INVENTION: AUGUST
CURRENT APPLICATION NUMBER: US/11/184,574
CURRENT APPLICATION NUMBER: US/110/029,840
PRIOR APPLICATION NUMBER: US/10/029,840
PRIOR APPLICATION NUMBER: US/10/029,840
PRIOR APPLICANTION TOWER: 201-12-31
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 483
                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                   119 VNSCARCFFHSVCPAGMIVKFPGTAOKNTVCEPASPGVSPACASPENCK----EPSSGTI 174
                                                                                                                                                                                                                                                                                                                                                                                               PQ--AKPTPVSPATSSASTMPVRG-GTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P---GIPHCCSRCHHGLF-NTHWRCSHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QEAGHAACSLILTQFVSSQALAELSTVMHQAWAKFDIRGHC----FCQVDARVWAPGDGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QOKEPTEKTPPTPQPSCNGDSNRTKDIKEETPDSTESPAE-----DGAGRSPLPCP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 EKDTTFEAPPLGTQPDCN------PTPENGEAPASTSPTQSLLVDSQASKTLPIP 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVTPALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSL--PLSPVRTRL 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPLMETCHSVGAAYLESLPLODASPAGGPSSPRDLPEPRVSTEHTN------NKIEK- 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 LRLSLWGMEA----LGTLGGQVQSLTAL-GPPQP----TNLDSTAFWEGFSHPETRPKL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VTQCQSC----VQAAGEVGVLTGHSQXSR------RSPLEEKQLEEEDSSATS 43
                                                                                                                                                                                                                                                                                                                                                                  EEGGGGPGPEASLNKGLAKHLLSGLGDRLCR----LLRKEREALAWAQREGQGPAMTEDS 99
                                                                                                                                                                                                                               209;
                                                                                                                                                                                    Length 595;
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                       SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
NUMBER OF SEQ ID NOS: 27
                                                                                                             ORGANISM: Homo sapiens
US-11-182-946-9
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373 ATRDSLRVFSSLCOIFSEEDNYSQSRELLVQEVKL---QSPLEPHSKKAPRSGSRGGGVV 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 VPMPPPRSSRRLRAGTLEALVRHLLDTRTSGTDVSFMSAFLATHRAFTS-TPALLGLMAD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 INLIPSOCLGGLWGHRDRPGH----SHLCPSVRATVTQFNKVAGAVVSSVLGATSTGE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 LGGQVQSLTALGPPQPTNL-----DSTAFWEGFSHP-ETRPKLDEGSVLLLHRTLGD 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 PYLGT-----FLKDLVMLDAASKDELENGYINFDKRRKEF-----AVLSELRRLQNEC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVFRAQDAQRIRRFLQMVCPAGAG-----TLEPGAPGSCYLDAGLRRRLREEWGVSCWTL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GGQQKEPTEKTPPTPQPSCNGDSNRTKDIKEETPDSTESPAEDGA-----GRS---- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----PSD--DRITNILDSIIAQVVER------KIQEKALGPGLRAGSG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 LRKGLSLPLSPVRTRLSP----- PGAL------ 351
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                                                                                                                         194 WFDSERVKAPLARLCSEIGA--PPSQKGSSSGMMMVAMRHLEGIARPKGGTGALTEA 248
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 -PLPCPSLCELLASTAVKLCLGH------DRIHMAFAPVTPAL----
                                                                                                643 HFLSPETSALSAQLCHQ-GASLPPDHR-----MLYAQMDRAVFQAVKAAVGALQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 5; 62; Mismatches 215; Indels 216;
                 PGSCYLDAGLRRRLREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTI--
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                                                                                                                                                                                                                                         Sequence 1658, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
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Best Local Similarity 20.1
Matches 124; Conservative
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US-10-821-234-1658
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                                                                                                                                             322
                                                                                                                                                                                                                              323 GLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQ 382
                                                                                                                                                                                                                                                                                                                                     442 LHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLASYLPLG---LTLHPLEPQLWAAYGV 498
                                                                                                                                                                                                                                                                                                                                                                                                                                   ------RDRVHKFTSDSP-------MAARLQDGTPQAALSPLTPR--KAPGP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 NSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLSGLDGEGLWSPGSQTSTVW 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IRRVRAQEIEAATLAGRLYSGRPNSGSREDSKGLAAHRLEQCEVPER-----EEQEQQ 167
                                                                                                                                                                                                                                                                                                           383 KTLRLSLWGMEALGTLGGQVQSLTALGPPQPT-NLDSTAFWEGFSHPETRPKLDEGSVLL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PCVLLQRLLLSG-----PSDTSSRFS 394
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                                                                                                    168 AEVSKPTPTP----EGTSQDVTTVTLLLRAPPGSTSS---SPASPSSSPTPASPEPPLE
                                                                                                                                                                                   220 PAEAQCL----TAEVPGSPEPPSPPKTTSPEPQESPTLPSTEGOVVNKLLSGPKETP
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                                                                                                                                               271 TAVKLCLGHDRIHMAFAPVTP-ALPSDDRITN-----ILDSIIAQVVERKIQEKALGP
                                                                                                                                                                                                                                                                       274 AAQ-----SPPRGPSDTKRAD-----VAGPRPCQ--------
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Fublication No. US20050251881A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours, Inc.

APPLICANT: Tao, Luan

TITLE OF INVENTION: CAROTENOID KETOLASE GENE

FILE REFRERNCE: CL-1849 US NA

CURRENT APPLICATION NUMBER: US/11/152,747

CURRENT FILING DATE: 2005-06-14

PRIOR FILING DATE: 2005-06-14

FRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Microsoft Office 97

SEQ ID NO 6
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2.4%; Score 90.5; DE
Best Local Similarity 27.1%; Pred. No. 2.9;
Matches 48; Conservative 20; Mismatches
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US-11-152-747-6
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Sequence 13-13-15
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Sequence 10-21-13-16
Sequence 10-21-15
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Sequence 10-21-15
Sequence 10-21-15
Septicant: Labet, Invention:
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
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134 YLDNECVHCE---EERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNTSSPRARCQPH 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 WMRHPSLCRKLGTLLKRHPEGEE-----SPPCPAPRADPHFPDLAEPLLP--MSGDLSP 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 ----PSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRITNILDSIIAQVVERKIQE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 KALGPGLRAGSGLRKGLSLPLSP-----VRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQ 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 SPAGP------PTAPSLEEVVLQQQSP---LVQARELEAEPGEHGQVAHGAN 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 CSRCHHGLFNTHWRCSHCSH-RLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACS
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                                                                                               APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US/10/186,643
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2000-07-02
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
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2.4%; Score 89; D
Best Local Similarity 19.9%; Pred. No. 2.
Matches 76; Conservative 51; Mismatche
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ORGANISM: Homo sapiens
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APPLICANT: Abraham, Elizabeth
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hizabeth
APPLICANT: Vallejo, Mario
TITLE OF INVENTION: BY ADMINISTERING A PSEUDO-ISLET LIKE AGGREGATE DIFFERENTIATED FR
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
FILE REFERENCE: 2084/12.3
CURRENT APPLICATION NUMBER: US 60/13, 255
PRIOR APPLICATION NUMBER: US 60/215, 109
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/239, 880
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
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PRIOR FILING DATE: 2000-10-06
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                                                                        ----EVLGSVGVP---TPLVSCDRPSTGGDEAPTTPAPLLTRLAQHMKWPSVSSLDSA 585
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   -TISVTQHFLSPETSALSAQ 655
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Best Local Similarity 23.5%; Pred. No. 14;
Matches 79; Conservative 23; Mismatches 121; Indels 113; Gaps
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614 LQAPGEAVLVPAGAPHQVQGLVS-
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10984645
Publication No. US20050244386Al
GENERAL INFORMATION:
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Publication No. US20050255100A1
                                                                                                                                                 667
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                                                                                                                                             656 L----CHQGASLPPDH
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US-10-984-645-2
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US-10-984-645-2
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US-11-182-946-6
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                                                                                                                                                                                     109 CHHGLF----NTHWRCSHCSHRLCVACGRIAGAGKNREKTGSQE----QHTDDCAQEAGH 160
                                                                                                                                                                                                             204 VWAPGDG---GQQKEPTEKTPPTPQPSCNGDSNRTKDI----KEETPDSTESPAEDGAG 255
                                                                                                                                                                                                                                                                                                                                     197 QAPPSYGQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AACSLILTQFVSSQAL------AELSTVMHQAWAKFDIRGHCFCQVDAR 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 127; Gaps
                                                            Query Match

2.4%; Score 88.5; DB 1; Length 419;
Best Local Similarity 21.1%; Pred. No. 3;
Matches 92; Conservative 45; Mismatches 172; Indels 12:
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385 HTAVLALEDEDDVLLV 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1556
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Search completed: November 25, 2005, 22:17:23 Job time : 14 secs

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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human mond mouse cDNA sequences.";

Prod. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: May act as a transcription factor that could act on to regulate one of the phases of hair growth.

-!- SUBCELLULAR LOCATION: Woclear.

-!- TISSUE SPECIFICITY: Expressed predominantly in brain, hair follicles and interfollicular epidermis. No expression in dermis.

-!- DISSABE: Defects in Hr are the cause of a number of pleiotropic effects including structural abnormalities of epithelial cells in the hair follicles, hair loss towards the end of the first hair
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1 VTQCQSCVQAAGEVGVLTGH......MDRAVFQAVKAAVGALQEAK 693
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O8k2j6
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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4QY90 MOUSE
AIR RAT
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QBWNL9 MACMU
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QGGS30_HUMAN
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Q9UPS0 HUMAN
Q6P9K3 MOUSE
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Q6ZQ57_MOUSE
Q68D47_HUMAN
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                    PubMed=15955095; DOI=10.1111/j.0022-202X.2005.23744.x; Zhang J.T., Fang S.G., Wang C.Y.; A Novel Nonsense Mutation and Polymorphisms in the Mouse
                                                                                                                                                                                                                                                                                                                                                                                           J. Invest. Dermatol. 124:1200-1205(2005).

EMBL, AX447391, AAT45233.1, -; mRNA.

MGI, MGI:96223; Hr.

SEQUENCE 1181 AA; 127068 WW; 53DEF4A87D8207BE CRC64;
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Pred. No. 3.6e-234;
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                                                                                                                    Q4QY90_MOUSE PRELIMINARY;
Q4QY90;
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STRAIN=KM; TISSUE=Skin;
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                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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 growth cycle, and the failure of subsequent hair growth cycles. Older mice carrying an hr mutation have been reported to possess altered ratios of T-cell-dependent B-cell responses. Mice homozygous for hr mutation are uniquely sensitive to UV and chemically induced skin tumors.
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EMBL; BC049182; AAH49182.1; -; mRNA.

PIK; 148378; 148378.

PIK; 148378; 148378.

MGI; MGI:96223; Hr.

InterPro; IPR003347; TF_JmjC.

PRAMT; SMOSS8; JmjC; 1.

DNA-binding; Metal-binding; Nuclear protein; Transcription;

Transcription regulation; Zinc; Zinc-finger.
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535 540 Poly-GJy.
401 401 P -> S (in Ref. 1).
1182 AA; 127193 MW; 3AFABE96CGEB3241 CRC64;
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99.4%; Pred. No. 2.1e-235;
tive 1; Mismatches 3;
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       TVMHQVWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPAPQLSCNGDSNRTKDIKE 728
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                                                     ETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRIT
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF3618641, AAL56245.1; -; mRNA.
InterPro; IPR003347; TF_JmjC.
Pfam, PF023173, JmjC, 1.
SEQUENCE 1187 AA, 127134 MW; DICFED4AAA76C77E CRC64;
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Pred. No. 2.8e-198;
3; Mismatches 68;
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Matches 582; Conservative 4:
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                              GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAGLRR
                                                                                                                           GLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAGLRR
                                                                                               RLREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLCHQG
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
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Ensembl; ENSRNGG0000011427; Rattus norvegicus.
InterPro; IPR003347; TF_UmjC.
InterPro373; UmjC; 1.
SWART; EM00558; UmjC; 1.
DNA-binding; Metal-binding; Nuclear protein; Transcription;
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94.8%; Score 3510; DB 1;
Best Local Similarity 95.1%; Pred. No. 5.5e-224;
Matches 659; Conservative 11; Mismatches 21;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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                                                                                                                                                                                              ASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK
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MEDLINE=97141510; Pubmed=8987811;
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SEQUENCE
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MEDLINES=9915-400; PubMed=10051399; DCI=10.1006/geno.1998.5699;
Ahmad W., Zlotogorski A., Panteleyev A.A., Lam H., Ahmad M.,
ul Haque M.F., Abdallah H.M., Dragan L., Christiano A.M.;
"Genomic organization of the human hairless gene (HR) and
identification of a mutation underlying congenital atrichia in an Arab
palestinian family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1] — WUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT ALUNC ALA-1022.
MEDLINE=99111413, PubMed=9445480, DOI=10.1126/science.279.5351.720, Ahmad W., ul Haque M.F., Brancolini V., Tsou H.C., Ul Haque S., Lam H., Aita V.M., Owen J., Deblaquiere M., Frank J., Geschalmi-Friedman P.B., Leask A., McGrath J.A., Peacocke M., Ahmad M., Ott J., Christiano A.M., "Alopecia universalis associated with a mutation in the human hairless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                       STVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIK
                                    EETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRI
                                                                             TNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPRP
                                                                                                                                TNILDSIIAQVVERKIQEKALGPGLRAGPGLRKGLGLPLSPVRPRLPPPGALLWLQEPRP
                                                                                                                                                       K--HGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD
                                                                                                                                                                                                STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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                                                                                                                                                                                                                                                                                      538 FLSGLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAG
  CPRCSHRLCVACGRVAGAGRAREKAGSREQSTEECTQEAGHAACSLTLTQFVSSQALAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE (ISOFORM 1), SEQUENCE REVISION TO 572 AND 774,
                                                                                                                                                                                                                                                                                                                                                                                               HOGPSLPPDCHLLYAQMDWAVFQAVKVAVGTLQEAK 1187
                                                                                                                                                                                                                                                                                                                                                                           658 HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                             043593; Q96H33; Q9NPE1; 15-UUL-1999 (Rel. 38, Created) 10-OCT-2003 (Rel. 42, Last sequence update) Hairless protein.
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NCBI_TaxID=9606;
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MEDLINE=2388257, PubMed=12477932; DOI=10.1073/pnss.242603899; MEDLINE=2388257, PubMed=12477932; DOI=10.1073/pnss.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., A pitchula S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., A bitchula S.F., John M.S., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., A sha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., McDan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A., Willahon D.K., Manay A.C., Shevchenko Y., Bouffard G.G., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., A blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., A blakealey R.W., Touchman J.W., Schwutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A blakealey R.W., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, genomic organization, alternative transcripts and mutational analysis of the gene responsible for autosomal recessive universal congenital alopecia.";
                                                                                                                                                                                                                                TISSUE=Brain, Fetal brain, and Peripheral blood leukocyte,
MEDLINE=98409496; PubMed=9736769; DOT=10.1093/hmg/7.11.1671;
Cichon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillmer A.,
Farcog S.A., Al-Dhafri K.S., Ahmad M., Haque S., Rietschel M.,
Propping P., Kruse R., Noethen M.M.;
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Hillmer A.M., Kruse R., Betz R.C., Schumacher J., Heyn U.,
Propping P., Noethen M.M., Cichon S.;
"Variant 18596->A (Arg620Gln) of the 'hairless' gene: absence
association with papular arrichia or androgenic alopecia.";
Am. J. Hum. Genet. 69:235-237(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 198-1189 (ISOFORM 3).
                                            Christiano A.M.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Comment=Additional isoforms seem to exist;
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IsoId=043593-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hum. Mol. Genet. 7:1671-1679(1998).
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MEDLINE=22294554; PubMed=12406339;
REVISION TO 446 AND 584
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1034 FLSGLDGEGLWSPGSQVSTVWHVFRAQDAQRIRRFLQMVCPAGAGALEPGAPGSCYLDAG 1093
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                                                                                                                                                                                                   Length 1189;
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                    /Fild=vAR 016222.

T -> A (in ALUNC).

/FILd=vAR 005266.

V -> D (in ALUNC).

/FILd=vAR 005267.

D -> G (in Ref. 4).

S -> L (in Ref. 5).

S -> L (in Ref. 5).
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hairless protein, isoform a.
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                                                                                                                                                                                               ; Score 3095.5; DB 1;
; Pred. No. 1.8e-196;
40; Mismatches 74;
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QGGS307
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                                                                                          TISSUE SPECIFICITY: Strongest expression of isoforms 1 and 2 is seen in the small intestine, weaker expression in brain and colon, and trace expression is found in liver, pancreas, spleen, thymus, stomach, salivary gland, appendix and trachea. Isoform 1 is always the most abundant. Isoform 1 is exclusively expressed at low levels in kidney and testis and isoform 2 exclusively at high levels in the skin.

DISBASE: Defects in HR are the cause of alopecia universalis congenita (ALUNC) [MIM:203655]. ALUNC is a rare autosomal recessive form of hair loss characterized by hair follicles
                                                                                                                                                                                                                                                                                       without hair.
DISEASE: Defects in HR are the cause of atrichia with papular
DISEASE: Defects in HR are the cause of atrichia atrichia. APL
lesions (APL) [MIM:209500]; also known as congenital atrichia. APL
is an autosomal recessive disease characterized by papillary
lesions over most of the body and almost complete absence of hair.
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LALRPLEPQLWAAYGV -> AGPGEHSQRHSALPLP (in
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GO; GO:0005634; C:nucleus, NAS.
GO; GO:0006355; P:transcription factor activity; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPRO33347; TF_JmjC.
Pfam; PF02373; JmjC; 1.
SMART; SMOGS58; JmjC; 1.
Allernative splicing; Disease mutation; DNA-binding; Metal-binding; Nuclear protein; Polymorphism; Transcription;
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/FTtd=VAR 005265.
D -> N (in ALUNC; affects binding to
                                                          IsoId=043593-3; Sequence=VSP 007990, VSP 007991;
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/FTId=VSP 007990.
Missing (In isoform 3).
/FTId=VSP 007991.
Missing (In isoform 2).
                                                                            Note=No experimental confirmation available;
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EMBL; AJ277249; CAB87577.2; -; Genomic_DNA.
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Name=2; Synonyme=Short;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNILDSIIAQVVERKIQEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPGALLWLQEPR- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - PKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALGTLGGQVQSLTALGPPQPTNLD 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 YLPLGLTLHPLEPQLWAAYGVNSHRGHLGTKNLCVEVSDLISILVHAEAQLPPWYRAQKD 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAEL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDASRVQNLVSSLPLPEYCAHQGKLNLAS
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Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTPPTPQPSCNGDSNRTKDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VTQCQSCVQAAGEVGVLTGHSQKSRRSPL-EEKQLEEEDSSATSEEGGGGPGPEASLNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EETPDSTESPAEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPVTPALPSDDRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.6%; Score 3095.5; DB 2; Length 1189;
83.2%; Pred. No. 1.8e-196;
ive 40; Mismatches 74; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC067128; AAH67128.1; -; mRNA.
SEQUENCE 1189 AA; 127494 MW; 67A4B95A01063387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Eukaryota, Metazoa,
Mammalia, Eutheria;
                                                                                                                                 NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
579; Conserv
                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWGMEALGTLGGOVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LWETEALGALGGQVHALTPLGPPQSTSLGSTAFWEGFSRPETRPKSDEGSVLLLHRALGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDASRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHPLEPQLWAAYGVNSHRGHLGTK
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                                                     FLSGLDGEGLWSPGSQTSTVWHVFRAQDAQRIRRFLQMVCPAGAGTLEPGAPGSCYLDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22755563; PubMed=12873232; DOI=10.1046/j.1365-2052.2003.010032.x; Pernandez A., Silio L., Noguera J.L., Sanchez A., Ovilo C.; "Linkage mapping of the porcine hairless gene (HR ) to chromosome 14.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     k; Score 1534; DB 2; Length 3
k; Pred. No. 1.5e-93;
15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovilo C.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY279972; AAP33389.1; -; mRNA.
InterProx; IPR003347; TF_JmjC.
Pfam; PP02373; JmjC; 1.
SMART; SM00558; JmjC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37147 MW; 35F00261F07B4A42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        693
                                                                                                                                                                                                   658 HQGASLPPDHRMLYAQMDRAVFQAVKAAVGALQEAK
                                                                                                                                                                                                                                                                                                                                 342 AA
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84.8%;
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Hairless (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.8
Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                16 PIG
QBG3E6_PIG PRELIMINARY;
Q863E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 3
342 AA;
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180 STVMHQAWAKFDIRGHCFC---QVDARVWAPGDGGQQ-------KEPTE 218
                                                                                                                                                                                                                                                                                                                                                             643 LDAMHTLREKYGIKSHCHCTUKQNLQVGNFPTMNGVSQVLQNVLNHSNKISLCMPESQQQ 702
                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SHÇSHRLÇVAÇGRIAGAĞKNREKTGSQEQHT-DDCAQEAGHAACSLILTQFVSSQALAEL 179
                                                                                                                                                                                                                                                                                                  587 QKCGFVVCLDCYK----AKERKSSRDKELYAWMKCVKGQPHDHKHLMPTQIIPGSVLTDL 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LG-TLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKD--- 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ASRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHP-LEPQLWAAYGVNSH 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TPALPSDDRITNILDSIIAQVVERKI------QEKALGPGLRAGSGLRKGL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 SLPLSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                936 ISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQKNKSGETVVLKL----KDWPS 991
                                                                                                                                                                                      61 AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 - PGSQTSTVWHVFRAQDAQRIRRFLOMVC-PAGAGTL---EPGAPGSCYLDAGLRRRLRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AEDGAGR-SPLPC----PSLCELLASTAVKLCLGHDRIHMAFAPV---
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                                                                                                                                                     Gapa
                                                                                                             Query Match
19.7%; Score 729; DB 2; Length 1265;
Best Local Similarity 29.2%; Pred. No. 1.9e-39;
Matches 219; Conservative 117; Mismatches 270; Indels 144;
                                                                            141291 MW; 33DB5BE53A7D9EBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 KTPPTPQPSCNGDSNRTKDIKEE ---TPDSTESP------
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Thyroid hormone receptor interactor 8.
Name=TRIP8; ORFNames=RP11-144G16.3-001;
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InterPro; IPR003347; TP_Jm
Pfam; PF02373; JmjC; 1.
SMART; SM00558; JmjC; 1.
NOW TER
SEQÜENCE 1265 AA; 14129:
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QSSQZ8;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SHCSHRLCVACGRIAGAGKNREKTGSQEQHTDDCAQEAGHAACSLILTQFVSSQALAELS
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MEDLINE-20181126; PubMed=10718198;
MABDLINE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes. XVI
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
EMBL; AB037801; BAA92618.1; -; mRNA.
                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.7%; Score 840.5; DB 2; Length 709; 70.1%; Pred. No. 3.8e-47; ive 16; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                        Finocchiaro R., Portolano B., Damiani G., Caroli A., Budelli Bolla P., Pagnacco G.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY13059; AAN05753.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75435 MW; 838EC14E3A1B0071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TVMHQAWAKFDIRGHCFCQVDARVWAPGDGGQQKEPTEKTP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAMHQVWVKFDIRGHCPCQADARVWTAGDGGLQKEPTEKTP 709
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Last annotation update)
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                     HOVOGLVSTISVTOHFLSPETSALSAOLCHOGASLP
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Matches 155; Conservative
                                                                                                                                            QBHZ76 SHEEP PRELIMINARY;
Q8HZ76;
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Q9P2G7;
                                                                                                                                                                                                                                        Hairless (Fragment).
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1864 VAAKDHDIGTTNLHIEVSDVVNILVYYGIAKGNGILSKAGILKKFEEEDLDDILRKRLKD 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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Chordata; Craniata; Vertebrata; Euteleostomi;
Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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19.7%; Score 728.5; DB 2; Length 2081;
Best Local Similarity 29.1%; Pred. No. 3.8e-39;
Matches 219; Conservative 118; Mismatches 267; Indels 149;
                                                                                                                                                Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AL713895; CA110948.1; -; Genomic DNA. EMBL, AL590502; CA110948.1; JOINED; Genomic_DNA. Ensembl; ENGS00000171988; Homo sapiens. GO; GO:0004872; F:receptor activity; IEA. InterPro; IFR033347; FF_JmjC. Pfam; PF02131; JmjC. SMART; SM00558; JmjC; 1.
                                                                                                                                                                                                                                                                                                                                                2081 AA; 231066 MW; 4DED8856C50CEDCE CRC64;
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                        Mammalia; Eutheria;
                                                                                                          NUCLEOTIDE SEQUENCE
                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| : || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STVMHQAWAKFDIRGHCFC----QVDARVWAPGDGGQQ-------KEPTE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AKHLISGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ASRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHP-LEPQLWAAYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 NSHRGH-LGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLSGLDGEGLWS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.7%; Score 728.5; DB 2; Length 2162; Best Local Similarity 29.1%; Pred. No. 4e-39; Matches 219; Conservative 118; Mismatches 267; Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ottenwaelder B., Obermaier B., Mewes H.W., Weil B., Wiemann Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL831917; CAD38578.1; -; mRNA.
Ensembl; ENSG00000171988; Homo sapiens.
InterPro; IPR00347; TF_JmjC.
Ffam; PF02373; JmjC; 1.
SMART; SM00558; JmjC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240377 MW; BFE6F0F68A957108 CRC64;
                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 KTPPTPQPSCNGDSNRTKDIKEE---TPDSTESP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 -TPALPSDDRITNILDSIIAQVVERKI------
                                                                                                01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence upd
01-0CT-2003 (TrEMBLrel. 25, Last annotation u
Mypochetical protein DKF2p761F0118 (Fragment)
Name=DKF2p761F0118;
     2162 AA
     PRT;
QBN3UO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein NON TER
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Amygdala;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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-DIPHSWICEK-----HILWLKDYKNSNNWKLFKECWKQGQPAVVSGVHKKMNISLWKAE 1110
                                                                                                                                                              1630 LDAMHTLREKYGIKSHCHCTNKONLOVGNPPTMNGVSQSQQONTPPKSEK--NGGSSPES 1687
                                                                                                                                                                                                                                                                                                                                                                                                             604 EEWGVSCWTLLQAPGBAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLCHQGASL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AKHLISGIGDRICRILRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AEDGAGR- 256
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                            394 ALG-TLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKD--
                                                                                                                                  --PGSQTSTVWHVFRAQDAQRIRRFLQMVC-PAGAGTL---EPGAPGSCYLDAGLRRRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SHCSHRLCVACGRIAGAGKNREKTGSQEQHT-DDCAQEAGHAACSLILTQFVSSQALAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 STVMHQAWAKPDIRGHCFCQVDARVWA---PGDGGQQKEPTEKTPPTPQPSCNGDSNRTK
                                                                                                                                                                                                                              501 HRGH-LGTKNLCVEVSDLISILVHAEAQLPPWYRAQKDFLSGLDGEGLWS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mews H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BX53/954; CAD97221.1; -; mRNA.
Ensembl; ENSG0000171988; Homo sapiens.
InterPro; IPR003347; TP_JmjC.
SPEam; PF02773; JmjC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.4%; Score 719; DB 2; Length 2210;
Best Local Similarity 30.0%; Pred. No. 1.8e-38;
Matches 207; Conservative 108; Mismatches 250; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245646 MW; B906415F74BBD690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1402 KEEINYDDKL---QVKNILYHAVKEMVRALK 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 PP----DHRMLYAQMDRAVFQAVKAAVGALQ 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Create 01-0CT-2003 (TrEMBLrel. 25, Last 8 01-MAR-2004 (TrEMBLrel. 26, Last 8 Hypothetical protein DKFZp686K091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 DIKEE---TPDSTESP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7Z3E7_HUMAN PRELIMINARY;
Q7Z3E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 protein.
2210 AA;
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SEQUENCE 22
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                                                                                                                                                       2061 LLEEYGVRTCTLIQFLGDAIVLPAGALHQVQNFHSCIQVTEDFVSPEHLVESFHLTQELR 2120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALPSDDRITNILDSIIAQVVERKI-------QEKALGPGLRAGSGLRKG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 LSLPLSPVRTRLSPPGALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGME 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
S
                     ----PGSQTSTVWHVFRAQDAQRIRRFLQMVC-PAGAGTL---EPGAPGSCYLDAGLRRR
                                                 LREEWGVSCWTLLQAPGEAVLVPAGAPHQVQGLVSTISVTQHFLSPETSALSAQLCHQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AKHLLSGLGDRLCRLLRKEREALAWAQREGQGPAMTEDSPGIPHCCSRCHHGLFNTHWRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 STVMHQAWAKFDIRGHCFC------QVDARVWAPGDGGQQKEPTEKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       878 NTPQKSEKNGGSSPESDVGTDNKLTPPESQSPLHWLADLAEQKAREEKKENKELTLENQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AEDGAGR-SPLPC-----PSLCELLASTAVKLCLGHDRIHMAFAPV----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR858245; CAH90482.1; -; mRNA.

InterPro: InterPro: IPR003347; TF_JmjC.

SPfam; PF02773; JmjC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1441 AA; 160281 MW; 704993D5EACC177C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    Ol-FEE-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp469A034 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 19.4%; Score 719.5; DB 2; Local Similarity 29.4%; Pred. No. 9.6e-39; es 221; Conservative 115; Mismatches 270;
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                                                                                                                                                                                                                              2121 LLKEEINYDDKL---QVKNILYHAVKEMVRALK 2150
                                                                                                                                                                                                  SLPP----DHRMLYAQMDRAVFQAVKAAVGALQ 690
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TISSUE=Kidney;
The German CDNA Consortium;
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NCBI_TaxID=9600;
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SEQUENCE
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Best Local S
Matches 221
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Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=20541717; PubMed=11087669; DOI=10.1006/geno.2000.6345;
Lai F., Godley L.A., Fernald A.A., Orelli B.J., Pamintuan L., Zhao N.,
Le Beau M.M.;
"CDNA cloning and genomic structure of three genes localized to human chromosome band 5q31 encoding potential nuclear proteins.";
                                                                                                                            SSGKGGRTMPNILDDIIASVVENKIP-----PNKTSKINIKSEPNEEPKESSLPATDESN
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                                                                                                                                                                                                                             KEE-TPDSTESP---AEDGAGRSPLPCPSLCELLASTAVKLCLGHDRIHMAFAPV---T
                                                                                                                                                                                                                                               PALPSDDRITNILDSIIAQVVERKIQEKALGPGLRAGSGLR-----KGLSLPLSPV--
                                                                                                                                                                                                                                                                                                                                                   342 RIRLSPPGA-----LLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEAL
                                                                                                                                                                                                                                                                                                                                                                                                               396 G-TLGGQVQSLTALGPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SRVQNLVSSLPLPEYCAHQGKLNLASYLPLGLTLHP-LEPQLWAAYGVNSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GH-LGTKNLCVEVSDLISILVH------AEAQLPPWYRAQK--DFLSGLDGEGLWS
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                                               121 SHCSHRLCVACGRIAGAGKNREKTGSQEQHT-DDCAQEAGHAACSLILTQFVSSQALAEL
                                                                                                                                                                     -----NGDSNRTKDI
                                                                                                                                                                                              ONSPOKSOTNGNSSPGSASTDSRLTPPESOSPLHWLADLAEOKSREEKQENKEFTLEREI
                                                                                                                                                                     OKEPTEK-------TPPTPQPSC-----
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTW-2003 (TrEMBLrel. 24, Last annotation update)
Putative zinc finger protein.
Homo sapiens (Human)
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                                                                                                            STVMHQAWAKFDIRGHCFC-----
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Q9nyf4;
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Mammalia, Eutheria;
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DVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLKDSSEIPGA----LWHIYAG 2091
      DVGTDNKLTPPESQSPLHWLADLAEQKAREEKKENKELTLENQIKEEREQDNSESPNGRT 1747
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A Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., A Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.,

Therdiction of the Coding Sequences of Mouse Homologues of KIAA Gene:

IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous

TONAS identified by Screening Of Terminal Sequences of cDNA Clones

TRandomly Sampled from Size-Fractionated Libraries.";

DNA Res. 11:205-218(2004).

R MGI: MGI:1918614; Jmjdc.

R MGI: MGI:1918614; Jmjdc.

R MGI: MGI:205-373; Jmdc; I.

R SMART; SM00558; Jmjc; I.
                                                                                              -----QEKALGPGLRAGSGLRKGLSLPLSPVRTRLSPPG 349
                                                                                                                                                                                                                                                                                                                                        DLISILVHAEAQLPPWYRAQKDFLSGLDGEGLWS------PGSQTSTVWHVFRA 563
                                                   350 ALLWLQEPRPKHGFHLFQEHWRQGQPVLVSGIQKTLRLSLWGMEALG-TLGGQVQSLTAL
                                                                                                                                                                                                                                                                            VSSLPLPEYCAHOGKLNLASYLPLGLTLHP-LEPQLWAAYGVNSHRGH-LGTKNLCVEVS
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                    SPLPC-----PSLCELLASTAVKLCLGHDRIHMAFAPV----TPALPSDDRITNILDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.0%; Score 702; DB 2; Length 2428;
.larity 28.7%; Pred. No. 2.6e-37;
Conservative 122; Mismatches 270; Indels 142;
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                                                                                                                                                                                                                  GPPQPTNLDSTAFWEGFSHPETRPKLDEGSVLLLHRTLGDKD
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Last annotation update)
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Name=Umjdlc; Synonyms=mKIAA1380;
Mus musculus (Mouse).
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Q69ZK6;
                                                                                              307 IAQVVERKI-----
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Matches 215; Conserv
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                                                                                                                                                                                                                                                                                                                                    239;
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Best Local Similarity 26.7%; Pred. No. 1.7e-37;
Matches 237; Conservative 120; Mismatches 291; Indels 239;
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                    EMBL, AF251039; AAF63765.1; -; mRNA.
InterPro; IPR007113; Cupin region.
InterPro; IPR003347; IF_JmjC.
Pfam; PF02373; JmjC; 1.
SMART; SM00558; JmjC; 1.
SEQUENCE 1417 AA; 154720 MW; E9CF503D8654FD2B CRC64;
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Search completed: November 25, 2005, 22:10:39 Job time: 240 secs

